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MPsrch\_pp Run on: protein - protein database search, using Smith-Waterman algorithm Tue Sep 26 16:16:03 2000; MasPar time 9.87 Seconds 731.891 Million cell updates/sec

Tabular output not generated.

Title: >US-09-308-435-2 (28-260) from US09308435.pep

Description: Perfect Score:

Sequence: 1 CSPHIIETNEVALKLNYHPA.....QKNLESYQKDAKELKGKRNR 233

Scoring table: PAM 150 Gap 11

Searched: 85661 seqs, 30989116 residues

Post-processing: Minimum Match 0% Listing first 45

summaries

Database: swiss-prot38 l:swissprot

Statistics: Mean 48.589; Variance 103.194; scale 0.471

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

2222 2322 242 252 252 252 252 252 252 252 252 2	Result No.
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	Pred. No.

EMBL; X92502; CAA63246.1; ..

ENBL; X92502; CAA63246.1; ..

PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.

PROSITE; PS00013; PROKAR\_LIPOPROTEIN; Signal.

BY SIMILARITY.

BY SIMILARITY.

Flagella; SIGNAL CHAIN LIPID

Query Match 100.0%; Best Local Similarity 100.0%; Matches 233; Conservative

Score 1594; DB 1; 1 Pred. No. 1.03e-279; 0; Mismatches 0;

Length 260; Indels

0

Gaps

0

SEQUENCE

260 AA; 29100 MW;

NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ.
N-ACYL DIGLYCERIDE (PROBABLE).
N-ACETYL-NEURAMINYL-ALPHA(2,3)-LACTOSE
BINDING MOTIF (POTENTIAL).
; F613B93FF1FF1F40 CRC64;

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## ALIGNMENTS

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	or send an email to license@ish-sih chi	entitles requires a license agreement (See http://www.ish-esh ch.commenced	modified and this statement is not removed IIsage by and for commercial		the European Bioinformatics Institute. There are no restrictions on its	between the Swiss Institute of Bioinformatics and the EMBL outstation -	This SWISS-PROT entry is copyright. It is produced through a collaboration		ANCHOR (PROBABLE).	-1- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY A LIDID	J. Bacteriol. 179:5643-5647(1997).	is not an adhesin for AGS cells.";	HpaA, a putative N-acetylneuraminyllactose-binding hemagglittinin. but	"A flagellar sheath protein of Helicobacter pylori is identical to	Jones A.C., Logan R.P., Foynes S., Cockayne A., Wren B.W., Penn C.W.:	MEDLINE; 97431527.	STRAIN-NCTC 11637;	SEQUENCE FROM N.A.	[1]	Helicobacter.	Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;	Helicobacter pylori (Campylobacter pylori).	HPAA.	BINDING SUBUNIT) (NLBH) (FLAGELLAR SHEATH ADHESIN).	ACETYLNEURAMINYLLACTOSE-BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR-	NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ PRECURSOR (N-	15-JUL-1998 (Rel. 36, Last annotation update)		01-NOV-1997 (Rel. 35; Created)		LT 1 HPA3 HELPY STANDARD: PRT: 260 A3

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Best Local :
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SIGNAL
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LIPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Tomb J.F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., McKenney K., Fitzgerald L.M., Feeterson J.D., Kelley J.M., Cotton M.D., Weidman J.M., Fijii C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Yenter J.C.;
                                                                                                                                                                                                                                                                                                                                                                          pylori.";
Nature 388:539-547(1997).
-i- SUBCELLULAR LOCATION:
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ PRECURSOR (N-ACETYLNEURAMINYLLACTOSE-BINDING FIBRILLAR HEMAGGLUTININ
                                                                                                                   SEQUENCE
                                                                                                                                                                                        PROSITE;
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MEDLINE; 97394467.
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                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                          "The putative neuraminyllactose-binding Helicobacter pylori CCUG 17874 is a lip J. Bacteriol. 177:6049-6057(1995).
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O'Toole P.W.,
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15-JUL-1998 (Rel. 36, Last annotation update)
NEURAMINYLACTOSE-BINDING HEMAGGLUTININ PRECURSOR
ACETYLNEURAMINYLLACTOSE-BINDING FIBRILLAR HEMAGGLU
                                                                                                                                                                              SEQUENCE
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                                                      EQILQNGGYKVINVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLF
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N-ACTYL DIGITCERIDE (PROBABLE).
N-ACTYL-NEURAMINYL-ALPHA(2,3)-LACTOSE
BINDING MOTIF (POTENTIAL).
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-i- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER M.
                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. These
use by non-profit institutions as long
modified and this statement is not removed.
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Bacteria; Proteobacteria; epsilon subdivision; Helicobacter
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01-NOV-1997 (Rel. 35, Last annotation update)
NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ PRECURSOR (N-
ACETYLNEURAMINYLLACTOSE-BINDING FIBRILLAR HEMAGGLUTININ
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embrane; Lipoprotein; Signal.
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BINDING MOTIF (POTENTIAL).
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HPAA_HELAC STANDARD;

047947;

047947;

01-NOV-1997 (Rel. 35, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

15-JUL-1998 (Rel. 36, Last annotation update)

15-JUL-1998 (Rel. 36, Last annotation update)

NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ (N-ACETYLNEURAMINYLLACTOSE-BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR-BINDING SUBUNIT) (NLBH)

ELIDING FIBRILLAR HEMAGGLUTININ RECEPTOR-BINDING SUBUNIT) (NLBH)
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NON_TER
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"Genetic evidence for host specificity "Genetic evidence for host specificity hnaA of
SEQUENCE FROM N.A.
MEDLINE; 96001251.
Evans D.G., Lampert H.C.,
Bronsdon M.A., Evans D.J.
                                                                                                         Helicobacter acinonyx.
Bacteria; Proteobacteria;
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-I- SUBCELLULAR LOCATION:
ANCHOR (PROBABLE).
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Helicobacter nemestrinae.
Bacteria; Proteobacteria;
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15-JUL-1998 (Rel. 36, Last annotation update)
NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ (N-ACETYLNEURAMINYLLACTOSE-BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR-BINDING SUBUNIT) (NLBH)
(FLAGELLAR SHEATH ADHESIN) (ADHESIN A) (FRAGMENT).
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embrane; Lipoprotein.
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No. 3.78e-133;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORC3_YEAST P54790;
                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 96239540. Hardy C.F.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ORIGIN RECOGNITION COMPLEX SUBUNIT 3 (ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetaceae;
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TE; PS00013; PROKAR_LII
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Pred. No. 2.
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2.63e-118;
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Query Match
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PHENYLALANYL-TRNA SYNTHERASE BETA CHAIN (EC 6
PRINA LIGASE BETA CHAIN) (PHERS).
PHET OR MF0049.
MYCOCAL---
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01-NOV-1997
01-NOV-1997
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or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
                                                                                                                                                                         Nucleic Acids Res. 24:4420-4449(1996).

1- CATALYTIC ACTIVITY: ATP + L-PHENYLALANINE
PYROPHOSPHATE + L-PHENYLALANYL-TRAKA(PHE).

-1- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BET
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-ATCC 29342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYFB_MYCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGD; L0003074; ORC3.

DNA replication; Nuclear protein; DNA-binding.

SEQUENCE 616 AA; 72077 MW; 3FAAEE3F645D3F9C
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EMBL; U48888; AAC49270.1; --
EMBL; X91488; CAA62765.1; --
EMBL; Z73109; CAA97447.1; --
SGD; L0003074; ORC3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homologous to the human cystic regulator protein CFTR."; Yeast 12:693-708(1996).
                                                                                                                                                                                                                                                                                                              Herrmann
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillo
Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma pneumoniae
                                                                                                                                                                                                                                                                 pneumoniae.
                                                                                                                                                                                                                                                                                                                              Himmelreich R.,
                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
                                                                                                                                                                                                                                                                                 'Complete sequence
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s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content ified and this statement is not removed. Usage by and
                                                                                                                                (BY SIMILARITY). SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                         (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: COMPONENT OF THE ORIGIN RECOGNITION COMPLEX (ORC) BINDS ORIGINS OF REPLICATION. IT HAS A ROLE IN BOTH CHROMOS REPLICATION AND MATING TYPE TRANSCRIPTIONAL SILENCING. BIND THE ARS CONSENSUS SEQUENCE (ACS) OF ORIGINS OF REPLICATION. SUBUNIT: ORC IS COMPOSED OF SIX SUBUNITS OF 120 KDA, 71 KDA KDA, 56 KDA, 53 KDA AND 50 KDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: NUCLEAR.
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26; Conser
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                                                                                                                                                                                                                                                                                                                                                       97105885
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larity 25.7%;
Conservative
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d. No. 4.42e-01;
Mismatches 32;
                                                                                                                                                                                                                                                                                     genome
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Best Local S
Matches
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Best Local Similarity
Matches 21; Conser
  MTNX_NEILA
P24581;
01-MAR-1992
01-MAR-1992
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YJI3_YEAST STANDARD; PKI; 1000 FA. 1024; P8.71924; P8.71924; P8.7192; Ol-FEB-1996 (Rel. 33, Created)
15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
TRANSPOSON TY4 207.7 NDA HYPOTHETICAL PROTEIN.
TY4B OR YJLLIAW OR JO780.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                        1171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cziepluch C., Kordes E., Pujol A., Jauniaux J.-C.; "Sequencing analysis of a 40.2 kb fragment of yeast chromosome X reveals 19 open reading frames including URA2 (5' end), TRK1, PBS2 SPT10, GCD14, RPE1, PHO86, NCA3, ASF1, CCT7, GZF3, two tRNA genes, three remnant delta elements and a Ty4 transposon."; Yeast 12:1471-1474(1996).
                                                                                                                                                                                                                                                                                                                                                                                                             Transposable SEQUENCE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z49389; CAA89409.1;
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MEDLINE; 97103775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aminoacyl-tRNA synthetase; SEQUENCE 805 AA; 91713 }
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183
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                                                                                                                                                                                                      DKNNSLTSYELERDKKRSKKNR 1252
                                                                                                                                                                                                                                            DISELDIQEKFIKTTHSSHSGGIVSTMVKGTDNSNDAI-KSA-LNKIFANI-MQEIDKKL 239
                                                                                                                                                                                                                                                                                   NIKELKYTDKNVPTDNGTNVSPRLEQNIEASGSPVQTVNKSAFLNKEFSSLNMKRKKKH 1230
                                                                                                                                                                TQKN-LESYQKDAKELKGKRNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 28.4%; 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        le element; Hypothetical protein.
1803 AA; 207693 MW; 16DCD7284A8D52D3 CRC64;
(Rel. 21, Created)
(Rel. 21, Last sequence update)
(Rel. 36, Last annotation updat
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                 STANDARD;
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25.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    584
                                                                                                                                                                260
                                                                                                                                                                                                                                                                                                                           Score 105; DB 1;
Pred. No. 7.61e-01
28; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 105; DB 1; Le
Pred. No. 7.61e-01;
21; Mismatches 33;
                                                                                 313
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                                                                                                                                                                                                                                                                                                                                                                 Length 1803
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Best Local S
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                                                                           STRAIN-NRRL Y-1094;
MEDLINE; 92380493.
Strick C.A., James L.C., O'Donnell M.M., Go
Strick Clain and characterization of the
The isolation and characterization of the
gene from the yeast Yarrowia lipolytica.";
Gene 118:65-72(1992).
                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PYRUVATE KINASE (EC 2.7.1.40)
Tarrowia lipolytica (Candida lipolytica).
Eukaryota, Fungi, Ascomycota; Saccharomyco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0105; C5METTRFRASE.
PROSITE; PS00094; C5_MTASE_1; 1.
PROSITE; PS00095; C5_MTASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and characterization of two ta
methyltransferase genes of Neisseria
M.NIaIII and a cytosine-type methylase.
Mol. Gen. Genet. 224:101-110(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-ATCC 23970 / NRCC MEDLINE; 91117164.
                                                                                                                                                                                                                                                                                                                                                                                    KPYK_YARLI
P30614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -I- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED CCNG, CAUSES SPECIFIC METHYLATION ON C-2 ON BOTH STRANI-I- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE.+ DNA CYTOS: S-ADENOSYL-L-HOMOCYSTEINE + DNA 5-METHYLCYTOSINE.
Strick C.A.,
                                     ERRATUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase; Methyltransferase; Restriction system.
ACT_SITE 74 74 BY SIMILARITY.
SEQUENCE 313 AA; 34842 MW; E75150C89ABEA611 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X54485; CAA38357.1; PIR; S12037; XYNHCL.
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                  MEDLINE; 94171073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QNRERIYLVGFLNHDVDFRFPQP 176
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PF00145; DNA_methylase;
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29; Conser
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larity 34.9%;
Conservative
  James
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                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
L.C.,
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  O'Donnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta subdivision; Neisseriaceae; Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 104; DB 1; Le
Pred. No. 9.95e-01;
18; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133
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                                                                                                                                                                                                                                                               Saccharomycetes;
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Gollaher
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pyruvate
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M.G.,
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Best Local (
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Q57775;
Q1-NOV-1997
Q1-NOV-1997
                           This SWI
between
the Euro
                                                                                                                                                           Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kalne B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BINDING
SEQUENCE
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       use
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MEDLINE; 96337999.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL
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                                                                                                                        Science 273:1058-1073(1996).
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                              European
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SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
SIMILARITY: BELONGS TO THE PYROVATE KINASE FAMILY.
                           SWISS-PROT entry is copyright. It is produ
een the Swiss Institute of Bioinformatics
European Bioinformatics Institute. There a
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O84533;
01-OCT 1996 (Rel. 34, Created)
01-OCT 1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTE TRNA LIGASE) (CYSRS).
TRNA LIGASE) (CYSRS).
TRNA LIGASE) (CYSRS).
SACCharomyces cerevisiae (Baker's yeast).
Saccharomyces cerevisiae (Baker's Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales;
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Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of an obligate intracellular pathogen of
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15-FEB-2000 (Rel.
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Local Similarity 23.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PASEKVQALDEKILLLRPAF-QYSD-NIAKEYENKFKNQTALK-VEQILQNQ-GYKVISV
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Similarity 36.7%;
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Pred. No. 1.69e+00;
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13; Mismatches
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Pred. No. 2.86e+00;
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Best Local Similarity 27.7%;
Matches 18; Conservative
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SEQUENCE FROM N.A.
STRAIN-S288C / FY1679;
MEDLINE; 97377992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF01406; tRNA-synt_1e; 1.

PRINTS; PR00983; TRNASYNTHCYS.

PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.

Hypothetical protein; Aminoacyl-tRNA synthetase; Protein biosynthesis;

Ligase; ATP-binding.

5 "HIGH" REGION.

SIMILAR 427 431 "KMSKS" REGION.

BINDING 430 430 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X96722; CAA65497.1; -.
EMBL; Z71523; CAA96154.1; -.
PFAM; PF01406; tRNA-synt_1e;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poehlmann R., Philippsen P.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-i- CATALYTIC ACTIVITY: ATP + L-CYSTEINE + TRNA(CYS) = AMP +
-YROPHOSPHATE + L-CYSTEINYL-TRNA(CYS).
-i- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sen-Gupta M., Gueldener U., Beinhauer J.D., Fiedler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 44-767 FROM N.A.
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       105
                                                                                                                                                                                                  101 QNVTDIDDKIILRARQNYLF-DNFVKENDTKFNATVVDKVKTALFQYINKNFTIQGSEIK 159
                                                                               160 TIEEF 164
                                                                                                                                                          49
       DKDDF 109
                                                                                                                                                          EKVQALDEKILL-LRPAFQYSDNIAKEYENKFKNQTALKVEQIL-Q--NQGYKVISVDSS 104
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430
767 AA;
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Pred. No. 2.20e+00;
16; Mismatches 26;
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ATP (BY SIMILARITY).
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

.Psrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Tue Sep 26 16:18:57 2000; MasPar time 8.99 Seconds 613.770 Million cell updates/sec

Title:

Description: Perfect Score: Sequence:

>US-09-308-435-4
(28-260) from US09308435.pep
1599
1 CSPHIIETNEVALKLNYHPA.....QKNLESYQKDAKELKGKRNR 233

Scoring table: PAM 150 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq36 1:geneseqp

Statistics: Mean 32.470; Variance 175.985; scale 0.185

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

22221111544321 2222223321	Result No.
1599 1589 1589 1589 1589 1589 1589 1589	Score
100.0 100.0	% Query Match
260 260 260 260 260 260 261 261 261 261 261 261 27 27 27 27 27 27 27 27 27 27 27 27 27	Length
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2.57e-113 2.57e-113 2.57e-113 2.57e-112 1.58e-112 3.20e-109 1.14e-108 5.74e-13 3.94e-08 3.94e-08 3.94e-08 3.94e-09 1.46e-07 5.19e-04 5.19e-04 5.19e-04 5.19e-04 5.19e-04 1.63e+01 1.63e+01 1.63e+01 2.86e+01 2.86e+01 4.33e+01 4.33e+01	No.

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ein sequ	XAP-1, part of the DNA	ca]	calci	0	_	Grapevine leafroll vir	Borrelia VS461 antigen	Corn derived pyruvate	Recombinant cold-resis	Petunia MADS box trans	Spinocerebellar ataxia	Human ataxin-2.	Spinocerebellar ataxia	Human heart muscle spe	Amino acid sequence of		⊆	Humanised C4Gl Ig heav	Fragment of humanised	Humanised C4G1 Ig heav	The second secon
									7.48e+01		٠	6.53e+01			:	6.53e+01	:	Ġ		6.53e+01	

## ALIGNMENTS

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	1599; D
	SQ Sequence 260 AA;
	use as a vaccine.
	CC for the diagnosis and treatment of H. pylori infections and for
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	Claim 2; Page 37-38; 49pp; 1
	PT prophylaxis or diagnosis of mammalian infections
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                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                            ps Disclosure; Page 35-36; 5lpp; English.

This polypeptide comprises a 29 kDa surface antigen which is compressed on the surface of both dividing (bacillary) and resting (colloid) forms of Helicobacter pylori. The antigen gives rise to both systemic and local (mucosal) production of antibodies. It is an adhesin that is conserved in all tested strains of H. pylori, and is also a putative virulence factor. The invention relates to a new pharmaceutical composition comprising a lipid aggregate of a negatively charged lipid or lipid mixture and at least one engatively charged lipid or lipid mixture and at least one antigenic, native or recombinant antigen of H. pylori, preferably the surface-exposed 29 kDa antigen, or a nucleic acid (see V34643) coding for such an antigen. The new formulations, which are useful as vaccine formulations, elicit a protective immune response against H. pylori infections, and are suitable for therapeutic and prophylactic use. An adequate response is produced even without adjuvant. A second, claimed 29 kDa antigen (see W60156) is provided that differs only at residue 222 (Ser for Arg).
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18-NOV-1997; SE1927.
22-NOV-1996; SE-004296.
(ASTR ) ASTRA AB.
Berglindh T, Lofroth J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aggregate of negatively charged lipid and Helicobacter pylori antigen - useful in therapeutic or preventative vaccines against both forms of bacterium, to generate systemic and mucosal antibody
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Helicobacter pylori 29 kDa surface-exposed antigen.
Cell surface antigen; adhesin; infection; vaccine;
Helicobacter pylori.
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                                                                                                                                                                                           TMYKGTDNSNDAIKRALNKIFANIMOEIDKKLTOKNLESYQKDAKELKGKRNR 260
                                                            STGLDKMEGVLIPAGFIKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGLVS
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TMVKGTDNSNDAIKRALNKIFANIMQEIDKKLTQKNLESYQKDAKELKGKRNR
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                                                                                                                                                EQILQNOGYKVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLF 147
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                                                                                                                                                                                                                                                                    ch 100.0%; Similarity 100.0%; 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; Protein;
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Pred. No. 2.57e-113;
0; Mismatches 0;
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W07449 stand W07449; 04-MAR-1997

standard; Protein; 260

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Antigen; therapy;

Helicobacter pylori

(first entry)

munogen; vaccine;

29

kDa antigen. immunisation;

Helicobacter

adhesin; immunogen; vaccine; diagnosis. cter pylori strain CCUG 17874 Location/Qualifiers

(NTCC

cleavage\_site

/label= Sig\_peptide 25. .28

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RESULTA

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PS Claim 6; Page 28-30; 51pp; English.
CC This polypeptide comprises a 29 kba surface antigen which is
CC expressed on the surface of both dividing (bacillary) and resting
CC (colloid) forms of Helicobacter pylori. The antigen gives rise to
CC both systemic and local (mucosal) production of antibodies. It is
CC and is also a putative virulence factor. The invention relates to
CC and is also a putative virulence factor. The invention relates to
CC anew pharmaceutical composition comprising a lipid aggregate of a
CC negatively charged lipid or lipid mixture and at least one
CC the surface-exposed 29 kDa antigen of H. pylori, preferably
CC coding for such an antigen. The new formulations, which are useful
as vaccine formulations, elicit a protective immune response
CC against H. pylori infections, and are suitable for therapeutic and
CC against H. pylori infections, and are suitable for therapeutic and
CC against H. pylori infections, and are suitable for therapeutic and
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Best Local 9
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Aggregate of negatively charged lipid and Helicobacter pyloriantigen - useful in therapeutic or preventative vaccines again both forms of bacterium, to generate systemic and mucosal ant
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Helicobacter pylori 29 kDa surface-exposed antigen.
Cell surface antigen; adhesin; infection; vaccine; drug delivery.
Helicobacter pylori.
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22-NOV-1996; SE-004296.
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Similarity 99.6%;
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Pred. No. 1.
0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Py Helicobacter pylori surface exposed antigen - useful for treatment, prophylaxis or diagnosis of mammalian infections sclaim 2; Page 34-35; 49pp; English.

Claim 2; Page 34-35; 49pp; English.

Claim 2; Page 34-35; 49pp; English.

Claim 2; Page 34-35; 49pp; English and dividing forms of the surface of resting and dividing forms of the bacterium. It is conserved in all tested strains of H. pylori, and gives rise to both systemic and local (mucosal) prodn. of antibodies. Its amino acid sequence was deduced from a cDNA clone (T43834); a sequence (W07550) deduced from a second cDNA clone (T43834); a sequence (W07550) deduced from a second cDNA clone (T43834); a sequence (W07550) deduced from a second cDNA clone (T43835) differs only at position 222 (Arg for Ser). Recombinant cantigen can be produced in transfer dost cells. It is useful for the diagnosis and treatment of H. pylori infections and for use as a vaccine.
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Best Local
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                                               26-NOV-1998
21-MAY-1997; 000091.
21-MAY-1997; WO-KR0091.
(DAEW-) DAEWOONG PHARM CO L
KIM BO, Lee BK, Park SK, Yo
WPI; 98-434925/37.
N-PSDB; X21955.
Fusion gene consisting of the Helicobacter pylori adhesin ligated to the A2 and B subunit gene of Vibrio cholerae to useful in the diagnosis and treatment of H. pylori Claim 2; Page 20-21; 32pp; English.
                                                                                                                                           duodenal ulcer.
Chimeric - Helicobacter pylori.
Chimeric - Vibrio cholerae.
                                                                                                                      WO9853082-A1.
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Bolin I, Svennerholm A;
WPI; 97-034307/03.
                                                                                                                                                                                            Fusion gene; H.
                                                                                                                                                                                                       18-MAY-1999 (
Adhesin/V.chol
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05-DEC-1996.
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                                                                                                                                                                                subunit; B subunit;
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SE-001085.
                                                                                                                                                                                                        (first entry)
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larity 99.6%;
Conservative
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peptidase
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                                                                                                                                                                                            pylori
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i infection;
diagnosis;
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ase II in prolipoproteins"
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adhesin gene; V. cholerae to
vaccine; gastritis; gastric
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Best Local S
Matches 23
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28-OCT-1997; U19575.
14-JUL-1997; US-891928.
28-OCT-1996; US-739150.
06-DEC-1996; US-759739.
             Recombinant or substantially pure preparations of H. pylori polypepti are disclosed, together with the nucleic acids encoding them. In all, 73 ORFS are shown. The proteins are variously cell envelope proteins, secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at legent and the proteins or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the fusion protein of the invention, between the H. pylori adhesin gene, and the V. cholerae toxin A2 and B subunit genes This protein is used in the diagnosis of and as a vaccine against H. pylori, which is the main cause of gastritis and gastric/duodenal ulcers. It may also be used in the production of an anti-H. pylori antibody. Vectors containing the DNA sequence and E. coli strains containing if form the basis of a process to produce the protein, which consists of culturing the microorganism and obtaining the protein. The protein is an effective vaccine against H. pylori due to its excellent immunogenicity for H. pylori, stability within the stomach environment, and its ability to penetrate through the stomach mucous membrane to stimulate strains and the strains the strains the strains to settlement t
    Sequence
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Alm RA,
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Vaccine; probe
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Note: This sequence was in
major country equivalent t
                                                                                                                                                                                                                                                                                                    Helicobacter pylori nucleic acids and proteins - use products for the detection, prevention and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori.
                                                                                                                                                                                                                                                            Claims 27, 31; Page
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DB; X30467.
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11ap20714_4797137_f3_45 cell envelope protein.
12be; diagnostic; ORF; cell envelope protein;
12tein; cellular protein.
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KR97059278.
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No. 1.
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H. pylori
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                                                                                                                                                                                                                                                      Helicobacter pylori nucleic acid sequences and related prolypeptide(s) - useful for vaccines to treat or prevent H. pylori prolypeptide(s) - useful for vaccines to treat or prevent H. pylori protein.

Bisclosure; Page 1363-64; 1481pp; English.

This sequence represents a H. pylori protein.

This sequence represents a H. pylori protein.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds; useful as potential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial CC DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified CC and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                            Matches
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Matches 223; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 DEC-1996. 009122. 06-JUN-1996; U09122. 07-JUN-1995; US-487032. 01-APR-1996; US-630405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytoplasmic; vaccine; prevention; treatment; identification; binding compound; bacterium; bacteria; inhibitor; duodenal ulcer disease;
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Berglindh OT, Sm
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                       156
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                                                                                                                 CSPHIIETNEVALKLNYHPASEKVOALDEKILLLRPAFQYSDNIAKEYENKFKNOTTLKV 95
STGLDKWERVLIPAGFVKVTILKPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGLVS
                                                                     EEILQNQGYKVINVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STGLDKMERVLIPAGFVKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGLVS
                                                   EQILQNQGYKVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLF 147
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                                                                                                                                                                                                          h 96.3%;
Similarity 95.3%;
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                                                                                                                                                                                      Score 1540; DB 1;
Pred. No. 1.14e-108;
7; Mismatches 4;
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life cycle; activator;
chronic gastritis;
                                                                                                                                                                                        4.
                                                                                                                                                                                                                        Length 268;
                                                                                                                                                                               Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents an H. pylori derived protein, no further details are given in the specification.

Chearils are given in the specification sequences of the invention of the invention of the sequences.

Chearils are given in the specification of sequences, and corresponding proteins are considered to useful for generating vaccines for immunising subjects against H.

Chearils are given in the sequences, and corresponding proteins, are considered for generating vaccines for immunising subjects against H.

Chearils are given in the sequences, and corresponding proteins, are considered for inhibit expression of a gene from Helicobacter species in the sample.

Chearils are given in the sequences of these sequences are considered by a fragments were blunt-ended and ligated to unique complementary to the BstXI-cut pMPX vectors, while the overhang is not complementary. Therefore the linkers will not concatemerise nor construct a series of shotgun subclone libraries. The purified DNA samples were then
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 4
H. pylori derived protein.

Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.

Helicobacter pylori.
                                                                                                                                                          W20454 standard; protein; W20454; 29-JUL-1997 (first entry)
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Transmembrane; cytoplasmic; cell envelope; flagella; transport; secreted; periplasmic; chronic gastritis; duodenal ulcer diseas activator; inhibitor; bacterial life cycle; vaccine; immunise; detection; antisense; inhibition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequenced.
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N-PSDB; T77481.
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15-NOV-1995; US-561469.
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12-AUG-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The ORF/protein reference number for this the related specification, WO9640893.
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97 AA;
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larity 97.7%;
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Pred. No. 5.74e-
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PT Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter; Disclosure, Page 625; 1481pp; English.

The present sequence is a H. pylori derived protein, no further details are given in the specification.

The protein may be used in a vaccine to prevent or treat H. pylori C. The protein may be used in a vaccine to prevent or treat H. pylori C. Useful as potential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori (ATCC 55679) was determined from coverlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To condition the predicted coding regions defined by computer evaluation acid sequences predicted from various ORF were analysed for significant code and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide conduction, e.g. in E. coli hosts.
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27-MAR-1997; U05223.
06-DEC-1996; US-6258
29-MAR-1996; US-7587
29-MAR-1996; US-7386
28-OCT-1996; US-7386
28-OCT-1996; US-7386
(ASTR ) ASTRA AB.
Alm RA, Smith D;
WPI; 97-503122/46.
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19-DEC-1996.
06-JUN 1996; U09122.
07-JUN-1995; U5-487032.
01-APR-1996; US-630405.
Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection Claims 14,80; Page 653; 1145pp; English.

This sequence is a H. pylori cell envelope outer membrane protein of the protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors.

DNA and probes derived from it may be used for the identification of the compounds of the identification of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H. pylori ORF 01ae11010_40688_c2_38 cell envelope OMP. Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
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Similarity 97.7%;
43; Conservative
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US-761318.
US-625811.
US-758731.
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RF 01ae11010_40688_c2_38
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25-OCT-1996;
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 Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection claim 14; Pages 558-559; 1145pp; English.

This sequence is a H. pylori protein of unspecified function. This sequence is a H. pylori protein to prevent or treat H. pylori The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. DNA and probes derived from it may be used for the identification on the pylori in a sample and the diagnosis of H. pylori infection. Nuclear the pylori in a sample and the diagnosis of H. pylori infection. Nuclear the pylori in a sample and the diagnosis of H. pylori infection. Nuclear the pylori in the pylori in the pylori infection.
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WPI; 97-503122/46.
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29-MAR-1996;
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gastritis; diagnosis.
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01-APR-1998; U06371.

29-JUL-1997; US-902615.

01-APR-1997; US-833457.

24-JUN-1997; US-881227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and distribution of H. pylori-specific antigens. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli
                                                                                                                                                           WPI; 98-542293/46.
W-PSDB; X14051.
New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases
Claim 8; Page 455-456; 2054pp; English.
This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating thelicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastriits, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
(INMA) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
Al-Garawi A, Kleanthous H, Miller C, Oomen RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori. WO9843478-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H. pylori GHPO 1615 protein.
GHPO protein; Helicobacter i
peptic ulcer disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W98332 standard; Protein; W98332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISID-AIKRALIKIFANIMQEIDKKITQKNIESYQKDAKELKGKRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SV-S-QFKDVSEIPQDIKEKALLVLRMDGNVAI-LE-D-IVEE-SDA--L-S-E-EKVID 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLIPAGFIKVTILEPMSGESLDSFTMDLSEL-DIQEKFLKTTHSSHSGGLVS-TMV-KGT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VALKLNYHPASEKVQALDEK-ILLLRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 58; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 AA;
      14.2%;
llarity 25.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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larity 25.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection; gastroduodenal disease; gastritis;
Score 227; DB 1; L
Pred. No. 1.46e-07;
75; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 235; DB 1; Length 261;
Pred. No. 3.94e-08;
75; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      À
                                                            Length 249;
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Indels

23;

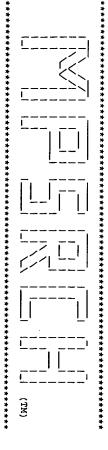
Gaps

22;

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-NSNDAIKRALNKIFANIMQEIDKKLTQKNLESYQKDAKELKG

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y10951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori nucleic acids and proteins products for the detection, prevention and trea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 ORFs are shown. The proteins are variously cell envelope proteins, secreted proteins or other cellular proteins. Vaccines containing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claims 27, 31; Page 151; 279pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 98-271811/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 ORFs are shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; X30418.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JUN-1999
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231 KNREDAIHKILNRMYAVVMKKAVTELTKENIAKYRDAIDRMKG
                                                                                                                                                                                                                    121 QVLRFQD-EKA-LNVQDKKKIFSVLDLKGWVGILEDLKMNL--K-DPN---SPNLDTL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152
                                                                                                                                                                           97
                                                                                                                                                                                                                                                                                           39
                                                                                                                                                                                                                                                                                                               64 PLDENY-PV-HIVQAPQNHHVVGILMPRIQVSDNL-KPYIDKFQDALINQIQTIFEKRGY 120 :| :| | | | | | | | : | :: :: | ::::|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143
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                                                                                                                                                                  KVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEG 156
                                                           VLIPAGFIKVTILEPMSGESLDSFTMDLSELD-
                                                                                                          VDQSSGSVWFNFYEPESNRVVHDFAVEVGTFQAITYTYTSTNNASGGFNSSKSVIHENLD
                                                                                                                                                                                                                                                                                  ALKLNYHPASEKVQA-LDEKIL-LLRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY 96
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                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
56; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probe; diagnostic; ORF;
protein; cellular protei
                                                                                                                                                                                                                                                                                                                                                                                                  11.0%;
llarity 25.1%;
Conservative
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; US-891928.
; US-739150.
; US-759739.
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                                                                                                                                                                                                                                                                                                                                                                                               Score 176; DB 1;
Pred. No. 5.19e-04;
59; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
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273
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of H. pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                          282;
                                                                                                                                                                                                                                                                                                                                                                                                  18;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Tue Sep 26 16:20:02 2000; MasPar time 9.81 Seconds 735.665 Million cell updates/sec

Description: Perfect Score: Title:

Sequence: >US-09-308-435-4 (28-260) from US09308435.pep 1599 1 CSPHITETRANSPORT CSPHIIETNEVALKLNYHPA.....QKNLESYQKDAKELKGKRNR 233

Scoring table: PAM 150 Gap 11

Searched: 85661 segs, 30989116 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 48.644; Variance 103.561; scale 0.470

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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97	98 97	99 100 100	100	103	109	848 771	1573	589	Score N
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Query Match 99.4%; Best Local Similarity 99.6%; Matches 232; Conservative

Score 1589; DB 1; Pred. No. 5.31e-278; 0; Mismatches 1;

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## ALIGNMENTS

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EMBL; X925 PROSITE; F Plagella; SIGNAL CHAIN LIPID DOMAIN SEQUENCE	This SWISS-PROT entroper the Swiss the European Bioinf use by non-profit modified and this sentities requires a or send an email to	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-NCTC 11637; STRAIN-, 97431527. JONES A.C., Logan "A flagellar sheat HpaA, a putative N 1s not an adhesin J. Bacteriol 179 -1- SUBCELLULAR LO ANCHOR (PROBAB	HPA3_HELPY STANI Q48261; 01-NOV-1997 (Rel. 3: 01-NOV-1997 (Rel. 3: 15-UTL-1998 (Rel. 3: NEURAMINYLLACTOSE-8: ACETYLNEURAMINYLLACT BINDING SUBUNIT) (NI HPAA. Helloobacter pylori Bacteria; proteobact Hellcobacter.
O 0 ⊢	This SWISS-PROT entry is coperated the European Bioinformatics use by non-profit institute the European Bioinformatics use by non-profit institute the European this statement and this statement entitles requires a license or send an email to license	SEQUENCE FROM N.A. STRAIN-NCTC 11637; MEDLINE; 97431527. JONES A.C., Logan R.P., Foynes S., "A flagellar sheath protein of Hel "A flagellar sheath protein of Hel Hpah, a putative N-acetylneuraminy is not an adhesin for AGS cells."; J. Bacteriol. 179:5643-5647(1997) J. Bacteriol. 179:5643-5647(1997) ANCHOR (PROBABLE).	T 1  HPA3_HELPY STANDARD; Q48261; Q148261; Q1-NOV-1997 (Rel. 35, Las 15-JUL-1998 (Rel. 35, Las NEURANINYLLACTOSE-BINDING ACETYLNEURANINYLLACTOSE-BINDING SUBUNIT) (NLBH) (HPAA. Helicobacter pylori (Camp Bacteria; Proteobacteria; Helicobacter.
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Nature 388:539-547(1997).
- SHRCELLULAR LOCATION:
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MEDLINE; 97394467.

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Pleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A. Rleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A. Relschmann R.D., Dodson K., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson K., Khalak H.G., Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M. Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M. Berg D.E., Gocayne J.M., Fujii C., Bowman C., Watthey L., Wallin Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Venter J.C.;
                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                        EMBL; AE000591; AAD07844.1; -.
TIGR; HP0797; -.
PROSITE; PS00013; PROKAR_LIPOP
Flagella; Outer membrane; Lipo;
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Bacteria; Proteobacteria; epsilon subdivision;
Helicobacter.
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PS00013; PROKAR_LIPOPROTEIN; 1.

Outer membrane; Lipoprotein; Signal.

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PS 260 AA; 29040 MW; D9F86C8B0556D071 CRC64;
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3; Outer membrane; Lipoprotein; Signal.

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Pred. No. 7
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W-ACYL DIGLYCERIDE (PROBABLE).
N-ACETYL-NEURAMINYL-ALPHA (2,3)-LACTOSE
BINDING MOTIF (POTEMYIAL).
; 676DDA952E99E03C CRC64;
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subdivision;
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Best Local
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      HPAA_HELNE
Q48244;
Q1-NOV-1997
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LIPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning, nucleotide sequence, and expreadhesin subunit protein of Helicobacter J. Bacteriol. 175:674-683(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ PRECURSOR (N-
ACETYLNEURAMINYLLACTOSE-BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR-
BINDING SUBUNIT) (NLBH) (FLAGELLAR SHEATH ADHESIN).
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Evans D.G., Karjalainen T.K., Evans D.J., Gran
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                                                                                                                                                                              STGLDKWEGVLIPAGFVKVTILEPMSGESLDSFTMDLSELDIOEKFLKTTHSSHSGGLVS
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larity 95.3%;
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i. No. 1.73e-269;
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01-NOV-1997
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PROSITE; P
Flagella;
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DOMAIN
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
NEURAMINYLLACTOSE-BINDING HEWAGGLUTININ (N-ACTYLNEURAMINYLLACTOSE-
BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR-BINDING SUBUNIT) (NLBH)
(FLAGELLAR SHEATH ADHESIN) (ADHESIN A) (FRAGMENT).
SEQUENCE FROM N.A.
MEDLINE; 96001251.
Evans D.G., Lampert H.C.,
Bronsdon M.A., Evans D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-JUL-1998 (Rel. 36, Last annotation update)
NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ (N-ACETYLNEURAMINYLLACTOSE-BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR-BINDING SUBUNIT) (NLBH)
(FLAGELLAR SHEATH ADHESIN) (ADHESIN A) (FRAGMENT).
                                                                                                                                 Helicobacter acinonyx.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wedline; youngert H.C., Nakano H., Ea Evans D.G., Lampert H.C., Nakano H., Ea Bronsdon M.A., Evans D.J. Jr.;
"Genetic evidence for host specificity genetic evidence for host specificity hnaA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 163:97-102(1995).
-!- SUBCELLULAR LOCATION:
ANCHOR (PROBABLE).
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Bacteria; Proteobacteria;
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TE; PS00013; PROKAR_LIPOPROTEIN;
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120; Conser
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  Nakano
Jr.;
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Pred. No. 8.64e-133;
4; Mismatches 1;
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                  Η.,
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PROSITE;
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MEDLINE; 96337999.
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PROTEIN MJ0329.
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                                                                                                                                                                                                                                 Miosga I., Zimmermann F.K.;

"Sequence analysis of the CEN12 region of Saccharomyces cerevisiae on a 43.7 kb fragment of chromosome XII including an open reading frame homologous to the human cystic fibrosis transmembrane conductance regulator protein CFTR.";

I yeast 12:693-708(1996).

I regulator protein CFTR.";

C regulator protein CFTR."

C I SUBCIONAL COMPONENT OF THE ORIGIN RECOGNITION COMPLEX (ORC) THAT BINDS ORIGINS OF REPLICATION. IT HAS A ROLE IN BOTH CHROMOSOMAL REPLICATION AND MATING TYPE TRANSCRIPTIONAL SILENCING. BINDS TO THE ARS CONSENSUS SEQUENCE (ACS) OF ORIGINS OF REPLICATION.

C I-SUBUNIT: ORC IS COMPOSED OF SIX SUBUNITS OF 120 KDA, 71 KDA, 62 KDA, 56 KDA, 53 KDA AND 50 KDA.

C I-SUBCELLULAR LOCATION: NUCLEAR.
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"The multidomain structure o
 of DNA replication and trans
Cell 83:563-568(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORC3 YEAST STANDARD; PRT; 616 AA p54790; O1-OCT-1996 (Rel. 34, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) ORIGIN RECOGNITION COMPLEX SUBUNIT 3 (ORIGI
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                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a coetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
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TIGR; MJ0329; -.
Hypothetical protein.
SEQUENCE 616 AA; 72036 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [3]
SEQUENCE FROM N.A.
FY23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 9623
Hardy C.F.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN 62 KDA SUBUNIT).
ORC3 OR OAF1 OR OIF1 OR YLL004W OR L1365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 96405918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Characterization of an essential Orc2p-associated factor that plays a role in DNA replication.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.,
MEDLINE; 96069857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Leber J., Kobayashi R., Stillman E ture of Orclp reveals similarity to transcriptional silencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARTIAL
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Pred. No. 2.
27; Mismatc
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1.68e-01;
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د.
                                                                                                                                                         collaboration
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Best Local :
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Best Local
                                                       Matches
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EMBL; U48888; AAC49270.1; -
EMBL; X91488; CAA62765.1; -
EMBL; Z73109; CAA97447.1; -
SGD; L0003074; ORC3
DNA replication; Nuclear pr
SEQUENCE 616 AA; 72077 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MTNX_NEILA
P24581;
01-MAR-1992
01-MAR-1992
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                     M.NIAIII and a cytosine-type methylase.";

Mol. Gen. Genet. 224:101-110(1990).

-I- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQ COMEG. CAUSES SPECIFIC METHYLATION ON C-2 ON BOTH STRANDS.

-I- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA CYTOSINE S-ADENOSYL-L-HOMOCYSTEINE + DNA 5-METHYLCYTOSINE.

-I- SIMILARITY: STRONG, TO OTHER C5-DNA METHYLASES.
                                                                                                                                                                                                                                                                               entities
or send a
                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a obstween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel.
CYTOSINE-SPECIFIC
                                                                                                                                                  PFAM; PF00145; DNA_methylase; 1.
PRINTS; PR00105; C5METTRFRASE.
PROSITE; PS00094; C5_MTASE_1; 1.
PROSITE; PS00095; C5_MTASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and characterization of two tandemly arranged DNA methyltransferase genes of Neisseria lactamica: an adenine-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-ATCC 23970
                                                                                                                        Transferase; Methyltransferase; Restriction system ACT_SITE 74 74 BY SIMILARITY.
                                                                                                                                                                                                                                     EMBL; X54485;
PIR; S12037; )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Labbe D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria
                                                                                                                                                                                                                           HSSP; P05102;
                                                                                                                                                                                                             REBASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 RILKRNYHKLDV-SSNKG-FKYGNQIFQSFLD-TVDGKLNL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 KDLAMVENEKDVDSINENTLDNEIILLKSAFKYDHVKISLIFNINTNLSNIEKNLRQSTI
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               ERILLAKKPQAFLL-ENV-KQLKGHDKGRT-LQVILAHLQQAGYKVYTEVLKARD-FGIP
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EKILLLR-P-AFQYSDNIAKEYENKFKNQTALKVEQI-LQNQGYKVISVDSSDKDDFSFA 112
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                                                                                                                                                                                                                                     2037; XYNHCL.
                                                      h 6.5%;
Similarity 34.9%;
29; Conservative
                                                                                                                                                                                                                                                                               an email to license@isb-sib.ch).
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                                                                                                              313 AA;
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larity 25.7%;
Conservative
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                                                                                                                                                                                                             M.Nlax.
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A; 72077 MW; 3F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21, Created)
21, Last sequence update)
36, Last annotation update)
METHYLTRANSFERASE NLAX (EC
                                                                                                              34842 MW;
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                                                                                                                                                                                                                                                                                              License
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                                                   Score 104; DB 1; Lo
Pred. No. 1.04e+00;
18; Mismatches 27;
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                                                                                                                                                                                                                                                                                              agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subdivision; Neisseriaceae;
                                                                                                             E75150C89ABEA611 CRC64;
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3FAAEE3F645D3F9C CRC64;
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                                                                                                                                                                                                                                                                                            http://www.isb-sib.ch/announce/
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                                                      Indels
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Matches 2
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15-FEB-2000 (Rel. 35, Last sequence)
PHENYLALANYL-TRNA SYNTHETASE BETA CHTRNA LIGASE BETA CHAIN) (PHERS).
PHET OR MP049.
                                                                                                                                                                                                                                                                 KPC1_NEUCR STANDARD
P87253;
15-JUL-1999 (Rel. 38, C.
15-JUL-1999 (Rel. 38, L.
PROTEIN KINASE C-LIKE (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYFB_MYCPN
P75563;
                                                        Arpaia G., Macino G
"Molecular cloning
crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                               Submitted
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                               Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aminoacyl-tRNA
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Nucleic Acids
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STRAIN-ATCC 29342 / M129;
MEDLINE; 97105885.
                                                                                                                                                                                                                                              Neurospora crassa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Himmelreich R.,
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Bacteria; Firmicutes; Bacillus/Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     565 SLLRVIQK-NAAYKNKLGNIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYROPHOSPHATE + L-PHI
SUBUNIT: TETRAMER OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLDKMEGVLIPAGFIKVTILEPMSGESLDSFTM-DLSEL-DIQEKFLKTTHSSHSGGLVS 207
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Similarity 28.4%;
23; Conservative
(MAR-1997) to t
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805 AA; 91713 MW;
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                                                                                                                                                                                                                                                                                                       . 38, Created)
. 38, Last sequ
. 38, Last anno
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                                                                                                                                                                                                            Ascomycota;
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Last annotation updat
(EC 2.7.1.-).
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                                                                                    protein kinase C
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   ZINC-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein biosynthesis; Ligase; W; 937B7614E789547A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228
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Pred.
20; M
                            EMBL/GenBank/DDBJ databases
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.. No. 1.35e+00;
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ACT_SITE
SEQUENCE
                                                                                                      MEDLINE; 99000809.
Stephens R.S., Kalman S
Mitchell W.P., Olinger
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DOMAIN
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PFAM; PF000130; DAG_PE-bind; 2.

PFAM; PF00065; pkinase; 1.

PFAM; PF00433; pkinase_C; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP,

PROSITE; PS00108; PROTEIN_KINASE_DOM;

PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia
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                                                          Chlamydia trachomatis.";
Science 282:754-759(1998).
                                                                                                                                          STRAIN-D/UW-3
                                                                                                                                             SEQUENCE FROM N.A. STRAIN-D/UW-3/CX;
                                                                                                                                                                                                     RPLC OR RL3 OR CT528
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15-FEB-2000 (Rel.
15-FEB-2000 (Rel.
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                                                                                                                                                                            Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00479; DAG_PE_BINDING_DOMAIN; 2.
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                                                                                  Genome sequence of an
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                                                                                                                                                                                                                                                                                                                            102 DSSDKDDFS-FAQKKEGYLAVAMNGEIVLRPDPKR 135
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                       FUNCTION: THIS PROTEIN BINDS DIRECTLY TO PARTICIPATE IN THE FORMATION OF THE PEPT: THE RIBOSOME (BY SIMILARITY).
               SIMILARITY: BELONGS
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SIMILARITY:
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             THE L3P FAMILY OF
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28;
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ATP (BY SIMILARITY).
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L., Zhao
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P53852;
                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pochimann R., Philippsen P.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (CTIVITY: ATP + L-CYSTEINE + TRNA(CYS) - AMP
PYROPHOSPHATE + L-CYSTEINYL-TRNA(CYS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOY-1997 (Rel. 35, Last annotation update)
PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                EMBL; X96722; CAA65497.1; -.
EMBL; Z71523; CAA96154.1; -.
FFAM; FF01406; tRNA-Synt_Le; 1.
PRINTS; PR00983; TRNASYNTHCYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rowserve analysis of the 33 kb long region between ORC5 and SUII from the left arm of chromosome XIV from Saccharomyces cerevisiae."; Yeast 13:849-860(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
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                                                                                                                                                        Hypothetical
                                                                                                                                                                                    PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 44-767 FROM N.A.
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TE; PS00474; RIBOSOMAL_L3; FALSE_NEG
                                        tical protein; Aminoacyl-tRNA synthetase;
ATP-binding.
65 75 "HIGH" REGION.
427 431 "KMSKS" REGION.
430 430 ATP (BY SIMILARITY).
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Similarity 36.7%;
18; Conservative
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Pred. No. 2.97e+00
13; Mismatches 1:
"HIGH" REGION.
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ATP (BY SIMILARITY).
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Query Match

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Best Local Similarity 27.7%; Matches 18; Conservative

Pred. No. 2.29e+00; 16; Mismatches 26;

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160 TIEEF 164 ::| 105 DKDDF 109

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Best Local Similarity 29.9%;
Matches 20; Conservative
YJL3_YEAST STANDAKU;
P47024; P87192;
01-FEB-1996 (Rel. 33, Created)
15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
174-8000 Ty4 207.7 KDA HYPOTHETICAL PROTEIN.
TY4B OR YJL113W OR J0780.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetales;
Cacharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RBP2_PLAVB STAN
Q00799;
01-APR-1993 (Rel. 2
01-APR-1993 (Rel. 2
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between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
use by non-profit institutions as long as its content is
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SEQUENCE FROM N.A.
MEDLINE; 92315338.
Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.;
Galinski M.R., Medina protein complex of Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Malaria;
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Eukaryota; Alveolata; Apicomplex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
RETICULOCYTE BINDING PROTEIN 2 (FRAGMENT).
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Pred. No. 2.97e+00;
17; Mismatches 26
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                                                                                             1171 NIKELKVTDKNVPTDNGTNVSPRLEQNIEASGSPVQTVNKSAFLNKEFSSLNMKRKRKRH 1230
                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                     Transposable element; Hypothetical protein.
SEQUENCE 1803 AA; 207693 MW; 16DCD7284A8D52D3 CRC64;
                                                                                                                                                                                                                                                           EMBL; Z49389; CAA89409.1; -
                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
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MEDLINE; 97103775.
                                                                        183
   240
TOKN-LESYQKDAKELKGKRNR
                                    DKNNSLTSYELERDKKRSKKNR
                                                                        DLSELDIQEKFLKTTHSSHSGGLVSTMVKGTDNSNDAI-KRA-LNKIFANI-MQEIDKKL 239
                                                                                                                                            h 6.3%;
Similarity 24.4%;
20; Conservative
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28; 1
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Pred. No. 2.97e+00;
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Search completed: Tue Sep 26 16:20:13 2000 Job time : 11 secs.

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-	H-depend	m	hypothetical protein	syringomycin syntheta	regulatory protein -	phenylalaninetRNA l	probable membrane pro	hypothetical protein	nionyl-tRNA for	gmp synthase, cter do	Ig heavy chain V regi	TyB protein - yeast (	hypothetical protein	patatin-like protein	reticulocyte-binding		probable endopeptidas	probable membrane pro	sensory transduction	sulfite reductase hom	hypothetical protein
2.64e+01		2.64e+01				1.69e+01							1.34e+01	1.34e+01	1.07e+01	8.50e+00		8.50e+00	8.50e+00	8.50e+00	8.50e+00

# ALIGNMENTS

##molecule_type DN ##residues 1- ##cross-references	#journal #title #cross-referen #accession #accession	##residues ##cross-re ##experimen REFERENCE #authors	#journal Natu: #title The ( #cross-references   #accession E646; ##status ##status type		DATE ACCESSIONS REFERENCE ###################################	RESULT 1 ENTRY TITLE TITLE ALTERNATE_NAMES ORGANISM
_type_DNA 1-2,'T',4,'G',6-18,'T',20-61,'K',63-83,'T',85-88,'E', 90-99,'N',101-108,'F',110-111,'A',113-152,'L',154-179, 'LEWI' ##label_EVA1 'Erences_GB:X61574; NID:g732735	993) 175:674-68 1de sequence, a hesin subunit p	##residues 1-260 ##label TOM ##cross-references GB:AE000591; GB:AE000511; NID:g2313918; pID:g2313925; #TIGR:HP0797 ##experimental_source strain 26695 NCE A47052 thors Evans, D.G.; Karjalainen, T.K.; Evans Jr., D.J.; Graham,	#journal Nature (1997) 388:539-547 #title The complete genome sequence of the gastric pathogen #cross-references MUID:97394467 #accession E64619 #accession E04619 #accession bucleic acid sequence not shown; translation not shown ##status nucleic acid sequence not shown;	Sutton (G.G.; Fleischmann, R.D.; Ketchum, K.A.; ClayCur, K.M.), H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weddman, J.M.; Fujil, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes, W.S.; Bordovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.M.; Venter, J.C.	09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 26-Feb-1999 E64619; B47052; C47052; PC4088 A64520 F. White C. Forly P. Charles P. Charl	E64619 #type complete adhesin A - Helicobacter pylori (strains 26695 and 8826) flagellar sheath adhesin hpaA; N-acetylneuraminyllactose-binding fibrillar hemagglutinin receptor-binding subunit formal name Helicobacter pylori

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ACCESSIONS
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                                         *cross-references
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##status preliminary
##molecule_type DNA
##residues 'MR',204-218,'R',220,'LC',223-228,'RS',231-234,'M',
##residues 'MR',204-218,'R',243-255,'N',257-260 ##label EVA2
##cross-references GB:x61574; NID:g732735
                                                                                                                                                                                                                                                                                                                                                                                                                                                 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##experimental_source strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQILQNOGYKVISVDSSDKDDLSFSQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLF 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STGLDKMEGVLIPAGFVKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGLVS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQILQNQGYKVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.1%;
Similarity 98.7%;
                           A71800
Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D Doig, P.C.; Smith, D.R.; Noonan, B.; Guild, B.C.; deJonge B.L.; Carmel, G.; Tummino, P.J.; Caruso, A.; Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Trust, T.J.

Nature (1999) 397:176-180
Genomic sequence comparison of two unrelated isolates of th human gastric pathogen Helicobacter pylori.
                                                                                                                                                                                                                                                                                            #type complete
neuraminyllactose-binding hemagglutinin
Helicobacter pylori (strain J99)
#formal_name Helicobacter pylori
strain J99
                       C71896
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                                                                                                                                                                                                                                                             12-Feb-1999 #sequence_revision 12-Feb-1999 12-Feb-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetic evidence for host specificity in the adhesin-encoding genes hxaA of Helicobacter acinonyx, hnaA of H. nemestrinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43-61,'K',63-83,'T',85-88,'E',90-99,'N',101-108,'F', 110-111,'A',113-123,'I',125-166 ##label EVA3
 preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #region receptor binding #status predicted the 260 #molecular-weight 29040 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence extracted from NCBI backbone (NCBIN:123532)
NCBIP:123534); sequence inconsistent with the nucleotide translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence extracted from NCBI backbone (NCBIN:123532)
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Pred. No. 1.16e-237;
3; Mismatches 0;
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                                                                                                                             Vovis,
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RESULT

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                                                                                                                                             Query Match 52.9%;
Best Local Similarity 96.0%;
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 225; Conser
                                                                                                                                                                                                                                                                                                                                                    #journal #title
                                                                                                                                                                                                                                                                                                           #title Genetic evidence for host specificity in the adhesin-encoding genes has of Helicobacter acinonyx, hnas of H. nemestrinae and hpas of H. pylori.
                                                                                                                                                                                                                                                                                                   #accession
 163
                                                 103
                                                                                                                                                                                                                                                            ##molecule_type DNA
##residues 1-124 ##label
##cross-references GB:U27127
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##residues
1-260 ##label ARN
##cross references GB.AE001504; GI
##experimental_source strain J99
                       121 FVKV 124
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                                             SSDKDDLSFAQKKEGYLAVAMNGEIVLRFDPKRTIQKKSEPGLLFSTGLDKMEGVLIPAG 120
                                                                                            NYHPASEKVQALDEKILLLRPAFQYRDNIAKEYENKFKNQTTLKVEQILQNQGYKVINVD 60
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166
                                                                                                                                                                                              #region receptor binding #status
#length 124 #checksum 6484
                                                                                                                                                                                                                                     hnaA
                                                                                                                                                                                                                                                                                                                                                              A.P.; Bronsdon, M.A.
Gene (1995) 163:97-102
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HnaA protein
                                                                                                                                                                                                                                                                                                                                                                                                                         #formal_name Helicobacter nemestrinae
14-Nov-1995 #sequence_revision 08-Feb-1996 #text_change
18-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                  Evans, D.G.; Lampert,
                                                                                                                                                                                                                                                                                                   PC4089
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larity 96.6%;
Conservative
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#length 260 #molecular-weight 29199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #type fragment
  Helicobacter nemestrinae (fragment)
                                                                                                                                              Score 843; DB 2; L
Pred. No. 2.25e-113;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1564; DB 2;
Pred. No. 6.15e-235;
7; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                        ert, H.C.; Nakano, H.;
M.A.; Evans Jr., D.J.
                                                                                                                                                                                                                                                                        EVA
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                                                                                                                                                                    Length 124;
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                                                                                             102
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Matches
 Query Match
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##molecule_type DNA
                                                                                                                                                                        human gastric pathogen Helicobacter pylori.
#cross-references MUID:99120557
#accession E71865
                                                      #gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                              #variety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #title Genetic evidence for host specificity in the adhesin-encoding genes haak of Helicobacter acinonyx, hnak of H. nemestrinae and hpak of H. pylori pross-references MUID:96001251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #journal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103
                                                                                                       ##residues 1-249 ##label ARN ##cross-references GB:AE001526; G
                                                                                                                           ##residues
                                                                                                                                      ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 FIKV 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
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##cross-references GB:U27126
                                                                                       ##experimental_source strain
                                                                                                                                                             #status
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Similarity 85.5%;
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Nature (1999) 397:176-180
                                                                                                                                                                                                                             Genomic sequence comparison of two unrelated isolates of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable neuraminyllactose-binding hemagglutinin jhp0971
Helicobacter pylori (strain J99)
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strain J99
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A.P.; Bronsdon, M.A.; Evans Jr., D.J.
Gene (1995) 163:97-102
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                                  #length 249
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14-Nov-1995 #sequence_revision 08-Feb-1996 #text_change
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                                                                                                                                                            preliminary
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rth 124 #checksum 6624
 14.48;
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Helicobacter acinonyx (fragment)
                                #molecular-weight 28513
 Score
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Pred. No. 1.26e-100;
14; Mismatches 4:
                                                                                       J99
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 230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102
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    210
                                               199
                                                                                       152
                                                                                                                                  143
                                                                                                                                                                                                                                                                                                                                                                                                                                    ##cross-references GB:AE000557; GB:AE000511; NID:g2313514; PID:g2313516;
TIGR:HP0410
X #length 249 #molecular-weight 28349 #checksum 9957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type DNA
##residues 1-249 ##label TOM
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  V-KGTDNSND-AIKSALNKIFANIMOEIDKKLTOKNLESYOKDAKELKGKRN
                      VHRIKETDHDQAIRKIMNQAYHKVMVHITKELSKKHMEHYEKVSSEMK-KRK
                                                                                       DKMEGVLIPAGFIKVTILEPMSGESLDSFTMDLSEL-DIQEKFLKTTHSSHSGGLVS-TM
                                                                                                                                                                        QNQGYKVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGL 151
                                                                                                                                                                                                              ERKGYSV-S-QFKDASEIPQDIKEKALLVLRMDGNVAI-LE-D-IVEE-SDA--L-S-E- 142
                                                                                                                                                                                                                                                           ETNE-VALKLNYHPASEKVQALDEK-ILLLRPAFQYSDNIAKEYENKFKNQTALKVEQIL 91
                                                                                                                                                                                                                                                                                                      NTGESVELHFHY-PIKGKQEPKNSHLVVLIEPKIEINKVIPESYQKEFEKSLFLQLSSFL 93
                                                                                                                           EKVID-M-SSGYLNLNEVEPKSEDIIHSFGIDVSKIKAVIER-VEL-RRINSGGFVPKTF 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNSND-AIKSALNKIFANIMQEIDKKLTQKNLESYQKDAKELKGKRN 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -M-SSGYLNLNFVEPKSEDIIHSFGIDVSKIKAVIER-VEL-RRTNSGGFVPKTFVHRIK 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VALKLNYHPASEKVQALDEK-ILLLRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLIPAGFIKVTILEPMSGESLDSFTMDLSEL-DIQEKFLKTTHSSHSGGLVS-TMV-KGT 213
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                                                                                                                                                                                                                                                                                                                                                 h 13.9%;
Similarity 25.0%;
58; Conservative
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Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk,
H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush,
J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.;
McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.;
Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Wterback, T.R.;
Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.;
Fujil, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes,
W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
C.M.; Venter, J.C.
Nature (1997) 388:539-547
The complete genome sequence of the gastric pathogen
Helicobacter pylori.
eerences MID:97394467
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Helicobacter pylori (strain 26695)
#formal_name Helicobacter pylori
09-Aug-1997 #sequence_revision 15-Aug-1997 #text_
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                                                                                                                                                                                                                                                                                                                                                 Score 222; DB 2; Length 249; Pred. No. 6.09e-15; 74; Mismatches 77; Indels
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Best Local Similarity 25.1%;
Matches 56; Conservative
#journal
                                                                                                                                                                                                                                                           #authors
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i#residues
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#cross-references GB:AE001479; GI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 PLDFNY-PV-HIVQAPQNHHVVGILMPRIQVSDNL-KPYIDKFQDALINQIQTIFEKRGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVLRFQD-EKA-LNVQDKKKIFSVLDLKGWVGILEDLKMNL--K-DPN---SPNLDTL-- 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNREDAIHKILNRMYAVVMKKAVTELTKENIAKYRDAIDRMKG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLIPAGFIKVTILEPMSGESLDSFTMDLSELD-IQEKFLKTTHSSHSGGLVSTMVKGT-D
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                Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.;
Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk,
H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush,
J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.;
McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.;
Hickey, E. K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.;
Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.;
Fujii, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes,
W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
C.M.; Venter, J.C.
Nature (1997) 388:539-547
                                                                                                                                                                                                                                                                                                                                              #formal_name Helicobacter pylori
09-Aug-1997 #sequence_revision 0
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26695)
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#length 282 #molecular-weight 32075 #checksum 2233
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Helicobacter pylori (strain J99)
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Doig, P.C.; Smith, D.R.; Noonan, B.; Guild, B.C.; deJonge,
B.L.; Carmel, G.; Tummino, P.J.; Caruso, A.;
Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.;
Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
G.F.; Trust, T.J.
                                                                                                                                                                                                                                                                                                                          10-Oct-1997
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ll protein HP0492 – Helicobacter
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Pred. No. 5.00e-08;
58; Mismatches 91
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#accession D64581
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                                                                                                                                                                                                                                                               1230 DKNNSLTSYELERDKKRSKRNR 1251
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1-1802 ##label
##cross-references EMBL:U11581
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##residues 1-2
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Local Similarity 26.8%;
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hes 56; Conservation
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hypothetical protein PAB0993 - Orsay)
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submitted to the EMBL Data Library, the sequence of S. cerevisiae cosmid
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#formal_name Saccharomyces cerevisiae
05-May-1995 #sequence_revision 19-Oct-1995 #text_change
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#length 278 #molecular-weight 31947 #checksum 4354
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Pred. No. 1.00e+00;
27; Mismatches 29
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Pred. No. 9.69e-07;
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                                          Pyrococcus
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ORGANISM

#formal\_name

Pyrococcus abyssi

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##cross-references SGD:S0003927; MIPS:YLL004w #map_position 12L #molecular-weight 72076
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Query Match
Best Local Similarity
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Best Local Similarity 24.7%;
Matches 21; Conservative
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#journal
#title
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#accession S701
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                                                                                                                   ##residues 1:616 ##label MIW
##cross-references EMBL:X91488; NID:g1495203; PID:e199016; PID:g1495220
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1995
                                                                                                                                                                                                                                                                                                                                                                                               ##cross-references EMBL:273109; NID:g1360162; PID:e245444; PID:g1360163; MIPS:YLL004w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##cross-references GB:AJ248287; GB:AL096836; NID:g5458657; PID:g5458916
                                                                                                                                                                                                                                                                                                                                                                                 ##experimental_source strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 QEIDKKLTQKNLESYQKDAKELKGK 257
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ORC3 protein - yeast (Saccharomyces cerevisiae)
protein L1365; protein YLLO04w
#formal_name Saccharomyces cerevisiae
01-Aug-1995 #sequence_revision 24-May-1996 #text_change
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submitted to the EMBL Data Library, July 199
submoteries abyssi genome sequence: insights
Pyrococcus abyssi genome sequence:
                                                                                                                                                                                                                         S70572
                                                                                                                                                                                                                                                                Sequence analysis of the CEN12 region of Saccharomyces cerevisiae on a 43.7 kb fragment of chromosome XII including an open reading frame homologous to the human cystic fibrosis transmembrane conductance regulator protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the Protein Sequence Database, May 1996 S64746
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S64746; S70572
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Yeast (1996) 12:693-708
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#length 320 #molecular-weight 37677
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 6.7%;
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 Score 107;
Pred. No.
 2.07e+00;
                Length 616
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REFERENCE
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Matches
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ALTERNATE_NAMES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type DNA
##residues 1-394 ##label KLE
##cross-references GB:AE001137; GB:AE000783; NID:g2688160; PID:g2688181;
##cross-references GB:AE00285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 DPKRTIQKKSEPGLLFSTGLDKMEGVLIPAGFIKVTILEPMSGESLDSFTMDLSELDIQE 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257 RLLKRNYHKLDY-SSNKG-FKYGNQIFQSFLD-TVDGKLNL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 EYENKFKNQTALKVEQILQNQGYKVISVDSSDKDDFSFAQK-KE-GYLAVANNGEIVLRP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                     KF 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 6.6%;
Similarity 19.7%;
24; Conservative
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                                                                                          26-Feb-1997 #sequence_revision
                                                                                                                                                                                             $73374 #type complete
phenylalanine-tRNA ligase (EC 6.1.1.20) beta chain pheT -
MYCOPlasma pneumoniae (APCC 29342) (SGC3)
hypothetical protein C09_orf805; phenylalanyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.; Dodson, R.; Hickey, E.K.; Gwinn, M.; Dougherty, B.; Tomb, J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, R.V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman, J.; Utterback, T.; Watthey, L.; McDonald, L.; Artiach, P.; Bowman, C.; Garland, S.; Fujil, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.; Smith, H.O.; Venter, J.C. Racure (1997) 390:580-586
  Himmelreich, R.;
                                                                                                                                                 #formal_name Mycoplasma pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #135 #type complete flagellar protein (flbC) homolog - Lyme disease spirochete formal_name Borrelia burgdorferi #common_name Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-Feb-1998
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                                                                             16-Jul-1999
                                                                                                                                                                             beta chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #sequence_revision 13-Feb-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 106; DB 2;
Pred. No. 2.63e+00;
44; Mismatches 48
  Hilbert,
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H.; Plagens,
                                                                                                  25-Apr-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 394
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H.;
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CLASSIFICATION
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##molecule_type DNA
##residues 1-1465 ##label JAN
##cross-references EMBL:S46865
                                                                                                                                                                                                                                                                                                                                                                                                                                                    latches
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                                                                                                                                                                                                                                                                                                                                        #mobile_element retrotransposon Ty4

MARY #length 1465 #checksum 1908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #cross-references MUID:97105885
#accession 873374
                                                                                                                                                                                            183
                                                                                                                                                                                                              833 NLKELKYTDKNYPTDNGTNYSPRLEQNIEASGSPYQTYNKSAFLNKEFSSLNMKRKRKRH 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    565 SLLRVIQK-NAAYKNKLGNIF 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 GLDKMEGYLIPAGFIKVTILEPMSGESLDSFTM-DLSEL-DIQEKFLKTTHSSHSGGLVS 207
                                                                                                                                                    893 DKNNSLTSYELERDKKRSKKNR 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               506 ALQKLRTKLQTLGFHNVITYQLISPERARNFNLFGLSNLWEIKNP-LSNERSVLRVGLID 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##cross-references EMBL;AE000006; GB:U00089; NID:g1673695;
PIDN:AAB95696.1; PID:g1673698

##note the nucleotide sequence was submitted to the EMBL Data
Library, November 1996
                                                                                                                  240 TOKN-LESYQKDAKELKGKRNR 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 TMVKGTDNSNDAIKSALNKIF 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type DNA
1-805 ##label HIM
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                                                                                                                                                                                       DLSELDIQEKFLKTTHSSHSGGLVSTMVKGTDNSNDAI-KSA-LNKIFANI-MQEIDKKL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.68;
Similarity 28.4%;
23; Conservation
                                                                                                                                                                                                                                                               h 6.6%;
Similarity 25.6%;
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TyB protein - yeast (Saccharomyces cerevisiae)
retrotransposon Ty4 (fragment)
#formal_name Saccharomyces cerevisiae
18-Jun-1993 #sequence_revision 25-Apr-1997 #text_change
25-Apr-1997
S56894 #type complete
TyB protein - yeast (Saccharomyces cerevisiae)
retrotransposon Ty4.JL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #superfamily phenylalanine--tRNA ligase beta chain aminoacyl-tRNA synthetase; ligase; protein biosynthesis #length 805 #molecular-weight 91713 #checksum 4320
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SGC3
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Nucleic Acids Res. (1996) 24:4420-4449

Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S31262 #type fragment
TyB protein - yeast (Sacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary; nucleic acid sequence translation not shown
                                                                                                                                                                                                                                                               Score 105; DB 2;
Pred. No. 3.33e+00;
28; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 105; DB 2; Length 805; Pred. No. 3.33e+00; 21; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                 29; Indels
                                                                                                                                                                                                                                                                                                   Length 1465;
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Search completed: Tue Sep 26 16:15:47 2000 Job time: 19 secs.
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                                                                                                                                                                                                                                            Query Match 6.6%;
Best Local Similarity 25.6%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                        #mobile_element retrotransposon Ty4.JL
MARY #length 1803 #molecular-weight 207708 #checksum
                                                                                                                                                                                                                                                                                                                                                                    #map_position 10L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors
                                                                                                                                                                                   1171 NIKELKVTDKNVPTDNGTNVSPRLEQNIEASGSPVQTVNKSAFLNKEFSSLNMKRKRKRH 1230
                                                                                                                      1231 DKNNSLTSYELERDKKRSKKNR 1252
                                                                              240 TOKN-LESYOKDAKELKGKRNR 260
                                                                                                                                                            183 DLSELDIQEKFLKTTHSSHSGGLVSTMVKGTDNSNDAI-KSA-LNKIFANI-MQEIDKKL 239
                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type DNA
##residues 1-18
                                                                                                                                                                                                                                                                                                                                                                                                          ##residues 1-1803 ##label CZI
##cross-references EMBL:Z49389; MIPS:YJL113w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein J0780; protein YJL113w
#formal_name Saccharomyces cerevisiae
08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cziepluch, C.; Kordes, E.; Pujol, A.; Jauniaux, J.C. submitted to the Protein Sequence Database, September 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S56894
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                                                                                                                                                                                                                                            Score 105; DB 2; L6
Pred. No. 3.33e+00;
28; Mismatches 29;
                                                                                                                                                                                                                                                                                    Length 1803;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Tue Sep 26 16:14:59 2000; MasPar time 9.09 Seconds 606.971 Million cell updates/sec

Description: Perfect Score: Title:

Sequence: >US-09-308-435-2 (28-260) from US09308435.pep 1594 1 CSPHIIETNEVALKLNYHPA.....QKNLESYQKDAKELKGKRNR 233

PAM 150 Gap 11

Scoring table:

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq36 1:geneseqp

Statistics: Mean 32.420; Variance 175.543; scale 0.185

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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	Result
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1594 1594 1589 1589 1589 1545 302 230 230 230 230 230 107 118 107 107 107 100 100	Score
100.0 100.0	Query Match
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W60156 W70449 W704450 W601456 W601456 W601456 W601456 W601456 W6015 W601	Ħ
Helicobacter pylori 29 Helicobacter pylori su Adhesin/V.cholerae tox Helicobacter pylori 29 Helicobacter lapzori 10 H. pylori derived prot H. pylori derived prot H. pylori ORF 01ae1101 H. pylori ORF 04ee1110 H. pylori GRPO 1615 pr H. pylori Secreted or H. pylori secreted or Grapevine leafroll vir ORC3 subunit of yeast S. cerevisiae origin o Human heart muscle spe Helicobacter ClpB (N-t Merozoite apical-end p Merozite apical-end-lo Pasteurella multocida	Description
4.75e-113 4.75e-113 1.18e-112 1.18e-112 1.18e-112 1.18e-110 3.45e-100 3.45e-100 3.45e-08 8.55e-08 8.55e-08 8.55e-08 8.55e-07 1.10e-03 1.10e-03 1.10e-03 1.10e+01 1.60	Pred. No.

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ь	ب	ب	4	М	μ	<b>ja</b>	Ь	Н	۲	-	μ,	1	Н	Н	H	<b>ja</b>	ш	ب	ب	ш	۳
R71011	W63145	R33553	R71015	W02616	R39266	W49814	W56319	W56322	R72386	W95018	W60213	W33807	W24800	W98549	W49816	R43339	W49818	R39268	W49817	R39267	W49813
neuronal	calcium ch	Sequence of the alpha	Human neuronal calcium	Wheat adenylosuccinate	Ig heavy-	id s		paragal	of th	×	Spinocerebellar ataxia		Spinocerebellar ataxia	מי	Amino acid sequence of		d seguer	Humanised C4G1 Ig heav	-	Humanised C4G1 Ig heav	Amino acid sequence of
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## ALIGNMENTS

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as vaccine formulations, elicit a protective immune response against H. pylori infections, and are suitable for therapeutic and prophylactic use. An adequate response is produced even without adjuvant. A second 29 kDa antigen (see W60157) is provided that differs only at residue 222 (Arg for Ser).		ylori, lates late of	Claim 6; Page 28-30; 51pp; English.  This polypeptide comprises a 29 kDa surface antigen which is expressed on the surface of both dividing (bacillary) and resting (colloid) forms of Helicobacter pylori. The antigen gives rise to both systemic and local (mucosal) production of antibodies. It is		M60156; standard; Protein; 260 AA. W60156; Standard; Frotein; Standard;

ğ 밁 Query Match 100.0%; Best Local Similarity 100.0%; Matches 233; Conservative Score 1594; DB 1; Length 260; Pred. No. 4.75e-113; 0; Mismatches 0; Indels Indels 0; Gaps

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Best Local
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05-DEC-1996; SE0727.
03-JUN 1996; SE-002007.
01-JUN-1995; SE-001085.
                                                                                                                                                                                                                                                                              Helicobacter pylori surface exposed antigen - useful for treatment, prophylaxis or diagnosis of mammalian infections
Claim 2; Page 34-35, 49pp; English.
A 29 kDa antigen (W07449) of Helicobacter pylori is an adhesin expressed on the surface of resting and dividing forms of the bacterium. It is conserved in all tested strains of H. pylori, and gives rise to both systemic and local (mucosal) produ. of antibodies. Its amino acid sequence was deduced from a cDNA clone (T43834); a sequence (W0750) deduced from a second cDNA clone (T43834); a sequence (W0750) deduced from a second cDNA clone antipen can be produced in transformed host cells. It is useful for the diagnosis and treatment of H. pylori infections and for
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Bolin I, Svennerholm
WPI; 97-034307/03.
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therapy;
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W07449
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CSPHIETNEVALKLNYHPASEKVQALDEKILLLRPAFQYSDNIAKEYENKFKNQTALKV
                                                STGLDKMEGVLIPAGFIKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGLVS
                                                                                                                 EQILQNQGYKYISYDSSDKDDFSFAQKKEGYLAVAMNGEIYLRPDPKRTIQKKSEPGLLF 147
                                                                                                                                                     CSPHILETNEVALKLNYHPASEKVQALDEKILLLRPAFQYSDNIAKEYENKFKNQTALKV
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Similarity 100.08;
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Location/Qualifiers
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be used in applns. of the invention"
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28. .260
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25. .28
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Relaim 2; Page 20-21; 32pp; English.

Chaim 2; Page 20-21; 32pp; English.

This sequence represents the fusion protein of the invention, between the third sequence represents the fusion protein of the invention, between the This sequence represents the diagnosis of and as a vaccine against the protein is used in the diagnosis of and as a vaccine against the pylori, which is the main cause of gastritis and gastric/duodenal culcers. It may also be used in the production of an anti-H. pylori antibody. Vectors containing the DNA sequence and E. coli strains containing it form the basis of a process to produce the protein, which consists of culturing the microorganism and obtaining the protein. The protein is an effective vaccine against H. pylori due to its excellent immunogenicity for H. pylori, stability within the stomach environment, and its ability to penetrate through the stomach mucous membrane to stimulate sigh production.
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Best Local S
Matches 23
                                                                                                 W60157; standard; Protein; 260 AA W60157; 28-SEP-1998 (first entry) Helicobacter pylori 29 kDa surfa Cell surface antigen; adhesin; i. Helicobacter pylori.
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21-MAY-1997; WO-KR0091.
21-MAY-1997; WO-KR0091.
(DAEW-) DAEWOONG PHARM CO
Kim BO, Lee BK, Park SK,
WPI; 98-434925/37.
                                               28-MAY-1998.
18-NOV-1997;
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Sequence 461 AA;
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Adhesin/V.cholerae toxin A2 and B subunit fusion p
Fusion gene; H. pylori infection; adhesin gene; V.
A2 subunit; B subunit; diagnosis; vaccine; gastrit
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Chimeric - Heli
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18-MAY-1999
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W74466 standard; Protein;
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l Similarity 100.0%;
233; Conservative
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Pred. No. 4.75e-11:
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22-NOV-1996;

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Best Local S
Matches 23
            W09638475-A1.
05-DEC 1996; SE0727.
03-JUN-1996; SE-002007.
21-MAR-1996; SE-001085.
(ASTR ) ASTRA AB.
Bolin I, Svennerholm A;
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therapy; diagnosis
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 o I, Svennerholm A;
97-034307/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 99.7%;
Similarity 99.6%;
232; Conservative
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                                                                                                                                                                                                                                                 pylori strain CCUG 178:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                          /note= "consensus recognition site peptidase II in prolipoproteins" 28. .260
                                                                                                                   /note-
be used
                                                                                                                                           /label=
                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                    /label= Sig_peptide
                                                                                                                                                                                                                                                                                              immunogen;
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"either the
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Pred. No. 1.18e-112;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                           kDa antigen.
immunisation; ulcer;
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Best Local S
Matches 23
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CA 29 kDa antigen (W07450) of Helicobacter pylori is an adhesin conserved in all tested strains of H. pylori, and gives rise to both systemic and local (mucosal) prodn. of antibodies. Its amino acid sequence was deduced from a cDNA clone (T43834) differs only at position 222 (Ser for Arg). Recombinant antigen can be produced in transformed host cells. It is useful for the diagnosis and treatment of H. pylori infections and for use as a vaccine.
          Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 73 OREs are shown. The proteins are variously cell envelope proteins, secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUN-1999 (first entry)
H. pylori ORF llap20714_4797137_f3_45 cell envelope protein.
Vaccine; probe; diagnostic; ORF; cell envelope protein;
secreted protein; cellular protein.
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Alm RA, Smith D;
WPI; 98-271811/24
                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori. WO9818323-A1.
 Sequence
                                                                                                                                                                                                                               Hellcobacter pylori nucleic acids and proteins - used products for the detection, prevention and treatment of
                                                                                                                                                                                                                                                                  WPI; 98-271811/24.
N-PSDB; X30467.
                                                                                                                                                                                                                                                                                                                                28-OCT-1997; U19575.
14-JUL-1997; US-891928.
28-OCT-1996; US-739150.
06-DEC-1996; US-759739.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; Protein;
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llarity 99.6%;
Conservative
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Pred. No. 1.18e-112;
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                                                                                                                                                                                                                                      Pf Helicobacter pylori nucleic acid sequences and related prolypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter Snglish.

Claim Scauence represents a H. pylori protein.

Claim Fertion or to identify H. pylori polypeptide binding compounds, competing the protein may be used in a vaccine to prevent or treat H. pylori claim fection or to identify H. pylori polypeptide binding compounds, competing sequence of H. pylori (ATCC 55679) was determined from coverlapping contigs generated by mechanically shearing the bacterial coverlapping contigs generated by mechanically shearing the bacterial contint of the sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To confort itself H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
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07-JUN-1995; US-487032.
01-APR-1996; US-630405.
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Cytoplasmic; vaccine; prevention; treatment; identification; binding compound; bacterium; bacteria; inhibitor; duodenal ulcer disease;
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STGLDKMERVLIPAGFVKVTILKPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGLVS 215
                                                                                                             CSPHIIETNEVALKLNYHPASEKVQALDEKILLLRPAFQYSDNIAKEYENKFKNQTALKV 87
                                             EQILQNQGYKVISYDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLF
                                                                 EEILQNQGYKVINVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLF 155
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95.7%;
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Pred. No. 3
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3.46e-109;
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life cycle; activator;
chronic gastritis;
                                                                                                                                                                                                           Length 268;
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CC Helicobacter pylori has been strongly linked to chronic gastritis and CC duodenal ulcer disease. The nucleic acid sequences of the invention CC are used to evaluate compounds, especially activators or inhibitors of CC bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequence. The nucleic acid sequences, and corresponding proteins, are CC sequence. The nucleic acid sequences, and corresponding proteins are CC used to inhibit expression of a gene from Helicobacter species in CC a sample. Antisense nucleic acid sequences of these sequences are used to inhibit expression of a gene from Helicobacter species. H. CC pylori whole genomic DNA was isolated and nebulised to a median size of Exti-linker adapters in 100-1000 fold molar excess. These linkers are CC complementary to the BstXI-cut pMPX vectors, while the overhang is not complementary. Therefore the linkers will not concatemerise nor CC will the cut vector re-ligate itself easily. The linker-adapter inserts were ligated to each of the 20 pMPX vectors to construct a series of construct as co
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Best Local S
Matches 4
H. pylori derived protein. Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor duodenal ulcer disease; chronic gastritis; diagnosis; envelope. Helicobacter pylori.
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W24663;
W24663;
12-AUG-1997
                                                                                                                                     W20454 standard;
W20454;
                                                                                                             29-JUL-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori nucleic acid sequences and related proteins used for diagnostics and therapeutics Claim 18; Page 178; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; cytoplasmic; cell envelope; flagella; transport; secreted; periplasmic; chronic gastritis; duodenal ulcer disease; activator; inhibitor; bacterial life cycle; vaccine; immunise; detection; antisense; inhibition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-NOV-1996; U18542.
17-NOV-1995; US-561469.
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larity 97.7%;
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Pred. No. 5.42e-13;
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Care given in the specification.

Care given in the specification.

Care protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, insertion or to identify H. pylori polypeptide binding compounds, insertion or to identify H. pylori polypeptide binding compounds, inserting the protein may be used in a vaccine to prevent or treat H. pylori (ATCC 55679) was determined from the genomic sequence of H. pylori (ATCC 55679) was determined from the genomic sequences were analysed for ORF of at least 180 nucleotides, in the sequences were analysed for ORF of at least 180 nucleotides, in the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
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Best Local S
Matches 4
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27-MAR-1997; U05223.
06-DEC-1996; US-761318.
29-MAR-1996; US-625811.
02-APR-1996; US-758731.
25-OCT-1996; US-736905.
28-OCT-1996; US-738859.
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19-DEC-1996.
06-JUN.1996; U09122.
07-JUN-1995; US-487032.
01-APR-1996; US-630405.
       Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection Claims 14,80; Page 653; 1145pp; English.

This sequence is a H. pylori cell envelope outer membrane protein (The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors.

DNA and probes derived from it may be used for the identification o
                                                                                                                                                                                                                                                                                                                                                 innibitor; duodenal ulcer
Helicobacter pylori.
W09737044-Al.
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H. pylori ORF Olael1010_40688_c2_38 cell envelope OMP.
Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacteria; life cycle; inhibitor; duodenal ulcer disease; chronic gastrifis; di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 10
W55445
                                                                                                                                                                               (ASTR ) ASTRA AB.
Alm RA, Smith D;
WPI; 97-503122/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori nucleic acid sequences and polypeptide(s) - useful for vaccines to treat infection, and to detect Helicobacter
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43; Conse
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larity 97.7%;
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i. No. 5.42e-13;
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09-OCT 1997; U05223.
27-MAR-1997; U05223.
06-DEC-1996; US-761318.
29-MAR-1996; US-625811.
02-APR-1996; US-73873.
25-OCT-1996; US-73805.
28-OCT-1996; US-738859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and distribution of H. pylori-specific antigens. The genomic sequence of H. pylori (AFCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli
     Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection.

Claim 14, pages 558-559, 1145pp, English.

This sequence is a H. pylori protein of unspecified function.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The pylori in a sample and the diagnosis of H. pylori infection. Nucle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
                                                                                                                                                                                                                       Alm RA,
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Alm RA, Smith
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Misc_difference 261
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W55332;
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Pred. No. 8.55e-08;
74; Mismatches 74
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                                                                                                                                                                                                                                                                                                                                                                                                    ding this amino specification"
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diagnosis.
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01-APR-1998; U06371.
29-JUL-1997; US-902615.
01-APR-1997; US-833457.
24-JUN-1997; US-881227.
                                                                                                           New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases Claim 8; Page 455-456; 2054pp; English.

This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also used for the production of antibodies. The products can also be used for the production of antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H. pylori GHPO 1615 protein.
GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis;
peptic ulcer disease.
Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and distribution of H. pylori-specific antigens. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amblificant in a pylori by PCR.
                                                                                                                                                                                                                                                                                                                                               (HDWA-) HUMAN GENOME SCI INC.
(INWA ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
Al-Garawi A, Kleanthous H, Miller C, Oomen RP,
WPI; 98-542293/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9843478-A1.
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31-MAR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 SV-S-QFKDVSEIPQDIKEKALLVLRMDGNVAI-LE-D-IVEE-SDA--L-S-E-EKVID 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 VELHFHY-PIKGKQEPKNNHLVVLIDPKIEANKVIPENYQKEFEKSLFLQLSNFLERKGY 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNSND-AIKSALNKIFANIMQEIDKKLTQKNLESYQKDAKELKGKRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLIPAGFIKYTILEPMSGESLDSFTMDLSEL-DIQEKFLKTTHSSHSGGLVS-TMV-KGT 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 14.4%;
Similarity 25.1%;
57; Conservative
                                                                                               249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 AA;
               13.9%;
Conservative
               Score 222; DB 1; Le
Pred. No. 3.15e-07;
74; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 230; DB 1;
Pred. No. 8.55e-08;
74; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₿
                                                   Length 249;
                                                                                                                                                                                                                                                                                                                                                                   Tomb
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                 Indels
               23;
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               Gaps
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 73 ORFs are shown. The proteins are variously cell envelope proteins, secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleic acids from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claims 27, 31; Page 151; 279pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine; probe; diagnostic; UKF; CE secreted protein; cellular protein.
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Y10951;
Y10951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  products for the detection, prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alm RA, Smith D;
WPI; 98-271811/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H. pylori ORF 04ee11108_3906963_f1_7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; X30418.
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Alm RA, Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUN-1999
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                                                                                                                                                                                                                                    121
231 KNREDAIHKILNRMYAVVMKKAVTELTKENIAKYRDAIDRMKG
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                                                                                                                                                                                                                                                                                39 ALKLNYHPASEKVQA-LDEKIL-LLRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY
                                                                                                                                                                                                                                                                                                                64 PLDFNY-PV-HIVQAPQNHHVVGILMPRIQVSDNL-KPYIDKFQDALINQIQTIFEKRGY : | : | | | | | | | : | : | ::::||
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                                                                                                         VDQSSGSVWFNFYEPESNRVVHDFAVEVGTFQAITYTYTSTNNASGGFNSSKSVIHENLD
                                                                                                                                                                    KVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEG
                                                                                                                                                                                                                   QVLRFQD-EKA-LNVQDKKKIFSVLDLKGWVGILEDLKMNL--K-DPN---SPNLDTL--
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                                                          VLIPAGFIKVTILEPMSGESLDSFTMDLSELD-IQEKFLKTTHSSHSGGLVSTMVKGT-D
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                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
56; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probe; diagnostic; ORF; cell envelope
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US-739150.
US-759739.
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                                                                                                                                                                                                                                                                                                                                                                                                                                10.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 171; DB 1; L
Pred. No. 1.10e-03;
58; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          $
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H. pylori
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PT infection, and to detect Helicobacter

PS Claim 72; Page 1333-1334; 1481pp; English.

CC The present sequence is a H. pylori secreted or periplasmic protein.

CC The protein may be used in a vaccine to prevent or treat H. pylori

CC infection or to identify H. pylori polypeptide binding compounds,

CC useful as potential H. pylori life cycle activators or inhibitors.

CC useful as potential H. pylori (ATCC 55679) was determined from

CC overlapping contigs generated by mechanically shearing the bacterial

CC not the sequences were analysed for ORF of at least 180 nucleotides,

CC identify likely H. pylori antigens for vaccine development, the amino

CC acid sequences predicted from various ORF were analysed for significant

CC homology to other known or exported membrane proteins. Having identified

CC and determined the sequences of interest, particular regions can be

isolated from H. pylori by PCR amplification for recombinant polypeptide

CC production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
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19-DEC-1996.
06-JUN-1996; U09122.
07-JUN-1995; US-487032.
                                                                                                                                   diagnosis.
Helicobacter pylori.
WO9640893-Al.
                                                                                                                                                                                                                                                                               H. pylori secreted or peripplsmic protein, 3906963.aa. Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activato bacteria; inhibitor; duodenal ulcer disease; chronic gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ASTR ) ASTRA AB.
Berglindh OT, Smith D,
WPI; 97-052306/05.
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06-JUN-1996; U09122.
07-JUN-1995; US-487032.
01-APR-1996; US-630405.
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Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
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W20468 standard; Protein; 147
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Local Similarity 25.1%;
hes 56; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
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gastritis;
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PR (ASTR ) ASTRA AB.
PI Berglindh OT, Smith D, Mellgaerd BL;
PR WPI, 97-052306/05.

DR WPI, 97-052306/05.

DR N-PSDB; T67633.

PT Helloobacter pylori nucleic acid sequences and related PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori PT infection, and to detect Helloobacter
PS Claim 72; Page 638; 1481pp; English.

CC The protein may be used in a vaccine to prevent or treat H. pylori CC infection or to identify H. pylori polypeptide binding compounds, CC useful as potential H. pylori life cycle activators or inhibitors.

CC The genomic sequence of H. pylori (ATCC 55679) was determined from coverlapping contigs generated by mechanically shearing the bacterial CC DNA. The sequences were analysed for ORF of at least 180 nucleotides, CC and the predicted coding regions defined by computer evaluation. To composite the predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified colored the sequences of interest, particular regions can be colored from H. pylori by PCR amplification for recombinant polypeptide sequence 147 AA;

Query Match 147; Score 118; DB 1; Length 147;
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Db 121 QVLRFQD-EKA-LNVQDKKKIFSVLDLKG 147
| : : | : : | : : : : : |
Qy 97 KVISVDSSDKDDFSFAQKKEGYLAVAMNG 125

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Search completed: Tue Sep 26 16:15:11 2000 Job time : 12 secs.

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                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TrembLrel. 05, Created)
01-JAN-1998 (TrembLrel. 05, Last sequence update)
01-NOV-1998 (TrembLrel. 08, Last annotation update)
PUTATIVE NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ HOMOLOG (HPAA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genomic-sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
EMBL; AE001526; AAD06549.1; -.
SEQUENCE 249 AA; 28513 MW; A3729951 CRC32;
                                                                                                                                                                                                                               STRAIN-26695
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   Helicobacter.
                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori (Campylobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VELHFHY-PIKGKQEPKNNHLVVLIDPKIEANKVIPENYQKEFEKSLFLQLSNFLERKGY
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Similarity 25.1%;
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Pred. No. 2.97e-19;
75; Mismatches 73; Indels
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Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A3729951 CRC32;
                                                                                                                                                                                                                                                                                                                     r pylori).
subdivision; Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence update) annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VOVIS G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOIG P.C.,
                           WALLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                    B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96
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RESULT 4
ID Q9ZLY2 PRELIMINARY; A
AC Q9ZLY2;
DT 01-MAY-1999 (TIEMBLITE1. 10, Cr
DT 01-MAY-1999 (TIEMBLITE1. 10, La
DT 01-MAY-1999 (TIEMBLITE1. 10, La
DT 01-MAY-1999 (TIEMBLITE1. 10, La
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SORRERRA
                                                                                                                                                                          Query Match 11.0%;
Best Local Similarity 25.1%;
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                "Genomic-sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
EMBL; AE001479; AAD06033.1; -.
SEQUENCE 282 AA; 32075 MW; E982253F CRC32;
                                                                                                                                                                                                                                                                                                                                  ALM R.A., LING L.-S.L., I
SMITH D.R., NOONAN B., GI
TUMMINO P.J., CARUSO A.,
                                                                                                                                                                                                                                                                                                                       GIBSON R., MERBERG D., MILLS S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 99120557.
                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori J99.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000557; AAD07478.1; -.
TIGR; HP0410; -.
Hypothetical protein.
SEQUENCE 249 AA; 28349 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JHP0444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pylori.";
Nature 388:539-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence
                                                                                                                                 210 V-KGTDNSND-AIKRALNKIFANIMQEIDKKLTQKNLESYQKDAKELKGKRN 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143
                                                                                                               39 ALKLNYHPASEKVQA-LDEKIL-LLRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 NTGESVELHFHY-PIKGKQEPKNSHLVVLIEPKIEINKVIPESYQKEFEKSLFLQLSSFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocal
                           VDQSSGSVWFNFYEPESNRVVHDFAVEVGTFQAITYTYTSTNNASGGFNSSKSVIHENLD
                                                       KVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEG
                                                                                    QVLRFQD-EKA-LNVQDKKKIFSVLDLKGWVGILEDLKMNL--K-DPN---SPNLDTL--
VLIPAGFIKVTILEPMSGESLDSFTMDLSELD-IQEKFLKTTHSSHSGGLVSTMVKGT-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VHRIKETDHDQAIRKIMNQAYHKVMVHITKELSKKHMEHYEKVSSEMK-KRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERKGYSV-S-QFKDASEIPQDIKEKALLVLRMDGNVAI-LE-D-IVEE-SDA--L-S-E- 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKMEGVLIPAGFIKVTILEPMSGESLDSFTMDLSEL-DIQEKFLKTTHSSHSGGLVS-TM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKVID-M-SSGYLNLNFVEPKSEDIIHSFGIDVSKIKAVIER-VEL-RRINSGGFVPKTF 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QNQGYKVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETNE-VALKLNYHPASEKVQALDEK-ILLLRPAFQYSDNIAKEYENKFKNQTALKVEQIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 14.2%;
Similarity 25.0%;
58; Conservative
                                                                                                                                                                                                                                                                                                                 , MOIR D.T., KING B.L., BROWN E.D., GUILD B.C., DEJONGE B.L., CARMEL G..., URIA-NICKELSEN M., MILLS D.M., IV MILLS S.D., JIANG Q., TAYLOR D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         epsilon
                                                                                                                                                                        Score 176; DB 2;
Pred. No. 3.63e-10;
59; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 227; DB 2;
Pred. No. 5.53e-18;
75; Mismatches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of
f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6BED3165 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathogen Helicobacter
                                                                                                                                                                                                     Length 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249;
                                                                                                                                                                                                                                                                                                                    IVES C.,
                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                DOIG P.C.,
                            230
                                                         156
                                                                                                                  96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91
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KNREDAIHKILNRMYAVVMKKAVTELTKENIAKYRDAIDRMKG

-NSNDAIKRALNKIFANIMQEIDKKLTQKNLESYQKDAKELKG

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QULT 6
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Sest Local Similarity 25.0%;
watches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998
01-JAN-1998
01-NOV-1998
SEQUENCE FROM N.A.
ALONSO J.C., LUDER G., STIEGE A.C., CHAI S., WEISE F., 1
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
EMBL; X97918; CA866554.1; -.
SEQUENCE . 179 AA; 20956 MW; 85120A6C CRC32;
                                                                                                                                                                                                                                                    048453;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
COMPLETE NUCLEONIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE: 97394467.

TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,
FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,
NELSON K., OUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,
NELSON K., OUACKENBUSH J., ZHOU L., KHALAK H.G., GLODEK A.,
MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.R.,
MCKENNEY K., FITZGERALD L.M., LE, N., ADAMS M.D., HICKEY E.R.,
BERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M.,
COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATTHEY L., WALLIN E.
HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
                                                                                                                                                                                                                               Bacteriophage SPP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 278 AA; 31947 MW; 79127867 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 388:539-547(1997).
EMBL; AE000564; AAD07568.1;
TIGR; HP0492; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VENTER J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHET ICAL
                                                                                                                                                                          ambda phage group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 VDQSSGSVWFNFYEPESNRVVHDFAVEVGTFQAM-TY-TYKHN-NSGGLNSSNSIIHEYL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 ALKLNYHPASEKVQA-LDEKIL-LLRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D-NSNDAIKRALNKIFANIMQEIDKKLTQKNLESYQKDAKELKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVLRFQD-EKA-LNAQDKRKIFSVLDLKGWVGILEDLKMNL--K-DPN---NPNLDTL-- 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKNKEDAIHKILNRMYAVVMKKAVTELTKENIDKYREAIDRMKG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLIPAGFIKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGL-VS-TMVKG-T 213
                                                                                                                                                                                                  dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TIEMBLIEL 05, Created)
(TIEMBLIEL 05, Last sequence update)
(TIEMBLIEL 08, Last annotation update)
L 31.9 KD PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 166; DB 2;
Pred. No. 1.05e-08;
62; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                  179 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256
                                                                                     TRAUTNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                       Query Match
Best Local s
Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O97281
O97281;
O97281;
O1-MAY-1999 (TIEMBLIEL 10, C
O1-MAY-1999 (TIEMBLIEL 10, I
O1-NOV-1999 (TIEMBLIEL 12, I
                                                                                                                                                                                                            CHARRON R.L., BARRY J.J., BU
Submitted (APR-1997) to the
EMBL; U97042; AAB581611; --
PFAM; PF00873; ACR_tran; 1.
PRINTS; PR00702; ACRIFLAVING
SEQUENCE 1027 AA; 110930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               006471
006471;
01-JUL-1997
01-JUL-1997
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-K61-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burkholderia cepacia (Pseudomonas cepacia).
Bacteria; Proteobacteria; beta subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CEOB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OLITER K., BOWMAN S., HARRIS D., LAWSON D., QUAIL M., B. Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases EMBL, AL034559; CAB39027.1; -
SEQUENCE 578 AA; 68384 MW; 1AC1C75C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum.
Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFC0895W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFC0895W PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
     119
                                                      405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 EYEKYKKKMKEKSMEMDMDNE 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 EKTNSLEETLYQINNEYNKCIDMIEKEIHDNIDDKESLKVKNELEKL-C-VIKKEKDEKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 DKK-LTQKNLESYQKDAKELKGKRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 EEKELVLRGMEQY-KEIKKIREEMN 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 SLDSFTMDLSELDIQEKFLKTTHSSHSGGLVSTMVKGTDNSNDAIKRALNKIFANIMQEI 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 SLDDIGQALSDMDIDEAFNQAFQALDNSGFFKRAVRAYWKKNDSIIKALESQ-AKTIEDV 146
                        IGIVVDDAIVVVENVERNIENGMNARQATIKA-MQEVSGPIIAIALTLIVAVFVPLAFMSG 463
LAVAMNGEIVLRPDPKRTIQK-KSEPGLLFSTGLDKMEGVLIPAGFIKVTILEPMS-GES 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DFS-FAQK-KEGYLAVAMNGE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKVQALDEKILLLRPAFQ-YSDNIAKEYENKFKNQTALKVEQILQNQGYKVISVDSSDKD
                                                                                                    h 7.3%;
Similarity 15.2%;
22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 7.3%;
Similarity 24.7%;
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TremBirel. 04, (TremBirel. 04, (TremBirel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                            ACRIFLAVINRP.
AA; 110930 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.7%;
                                                                                                                                                                                                                                                                                                    to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                    BURNS J.L.;
ne EMBL/GenBank/DDBJ databases
                                                                                                    Score 116; DB 2; Le Pred. No. 6.05e-02; 62; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 117; DB 5; Le
Pred. No. 4.55e-02;
22; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 139; DB 9; Le
Pred. No. 6.35e-05;
27; Mismatches 31;
                                                                                                                                                                                                            7C8108F2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1027 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burkholderia
                                                                                                                                                      Length 1027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                    Indels
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                                                                                                       œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ω
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107
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071192;
071192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF000252; AAB52934.1; -. HSSP; P03069; 2DGC. PPAM; PF00170; bZIP; 1. SEQUENCE 417 AA; 48317 MW; D71C1C08 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTLORE B., O'CALLAGHAN M.,
PARSONS J., PECY C., RIKKEN L., ROOPEA A., SAUNDERS D., SHOWNKEEN R.
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 MD of contiguous nucleotide sequence from chromosome III of C.
TELEBRAS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     002080
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
SIMILAR TO CCAAT/ENHANCER-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WAMSLEY P., KRAMER J.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Rhabditina; Rhabditoidea; Rhal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C48E7.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 368:32-38(1994).
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                                                                                                                             199 SSHSGGLVSTMVKGTDNSND-AIKRAL-NKIFANIMQEIDKKL 239
                                                                                                                                                                                                                                       140 KSEPGL-LFSTGLDKMEGVLIPAGFIKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTH 198
                                                                                                                                                                                157 LGELTVLMSKMMKGESITVEPSVKRALKHRVFIEKMKPVEDKM 199
                                                                                                                                                                                                                                                                      100 MTETEQEAFADLVAELETQTAEAVKAFSKVFDRME-EINDD-KEGLSLLKLKN-YEMTAY 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         464 LTGQFYKQFA-MTIAISTVISAFNSLTLSPALSAILLKGHGDKEDWLTRVMNRVLGGFFR 522
                                                                                                                                                                                                                                                                                                                                                              81
                                                                                                                                                                                                                                                                                                                                                                                                 43 NDTAEKYDELKKENETLERKYEQLQKE-LSFL--KEMFMAYAKNDGNDGPPPPPPPSSSA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 Match 7.18;
Local Similarity 24.58;
hes 40; Conservative
                                                                                                                                                                                                                                                                                                                                                NOTALKYEQILQNQGYKVISYDSSDKDDFSFAQKKEGYLAVAMN-GEIVLRPDPKRTIQK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDS-FTMDLSELDIQ-EKFLKTTHS-SHSGGLVSTMVKGTDNSNDAIKRALNKIFANIMQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIDKKLTQKNLESYQKDAKELKGKR 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GFNKVF-HRGAENYGRGVRGVLSRK 546
                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pda; Secernentea; Rhabditia; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 114; DB 5; Le
Pred. No. 1.07e-01;
42; Mismatches 71;
                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                            549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHOWNKEEN R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                       Query Match 6.7%;
Best Local Similarity 24.4%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.8%;
Best Local Similarity 24.5%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O85168 PRELIMINARY;
O85168;
01-NOV-1998 (TIEMBLICEL. C
01-NOV-1998 (TIEMBLICEL. C
01-NOV-1999 (TIEMBLICEL.)
                                                      4377 IRGRLIRMAEDHHVLLLTLHHIVSDGWSVDVLTRELSALYAAFSQDQDDPLAPLELQ-Y 4434
                                                                                                                                                          4322 MOGDDGQPVQRISPADTGFNLQMHDLQG-LADAE-EKLQAL-A-SEESLQSFDLQQGPL- 4376 :: | : | : | : | | | : : : |
                                                                                                                                                                                                                                                                                                                                                                                                       GUENZI E., GRANDI G.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF047928; AAC80285.1; -
PROSITE; PS00455; AMP_BINDING; 8.
PFAM; PF00501; AMP-binding; 8.
PFAM; PF00568; DUF4; 9.
PFAM; PF00550; pp-binding; 9.
PFAM; PF00575; Thioesterase; 1.
PFAM; PF00975; Thioesterase; 1.
PFINTS; PR00154; AMPBINDING.
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Nucleotide sequence of the 3'-terminal two-thirds of the grapevine leafroll-associated virus-3 genome reveals a typical monopartite closterovirus.";
J. Gen. Virol. 79:1299-1307(1998).
EMBL; AF037568; AAC40708.1;
SEQUENCE 549 AA; 59013 MW; 2B128E62 CRC32;
189 IQEKFLKTTHSSHSGGLVSTMVKGTDNSNDAIKRALNKIFANIMQEIDKKLTQKNLESY
                                                                                                                      129 LRPDPKRTIQKKSEPGLLFSTGLDKMEGVLIPAGFIKVTILEPMSGESLDSFTMDLSELD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas syringae (pv. syringae).
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYRINGOMYCIN SYNTHETASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 98264508.
LING K.-S., ZHU H.-Y., DRONG R.F., SLIGHTOM J.L., MCFERSON GONSALVES D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       grapevine leafroll-associated virus 3.
Viruses; ssRNA positive-strand viruses,
Closterovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUV-1998 (TrEMBLrel. 08, Last annotation updat
59 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 GFIKVTIL-E-PMSGESLDSFTMDLSELDIQEKFLKTT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 DSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEGVLIPA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     444 DPVETDVAQFNLSTDGTVSVIVNGEEV-KNEYLVFGTINVLDSLYVKSGREDLEAKAIPE 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       503 YLTTLNILHDKAFTRRNLGNKDKGFSDLRIEENFLKSA 540
                                                                                                                                                                                                                                                                                                                                                                              9376 AA; 1029826 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08,
12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                Score 107; DB 2; Length 9376; Pred. No. 7.37e-01; 33; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 109; DB 14;
Pred. No. 4.27e-01;
30; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                              E4B2CD95 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9376 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
247
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RESULT 12 ID 093582 AC 093582;

PRELIMINARY;

PRT;

387 AA

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  044769;
01-NOY-1996 (TremBLrel. 01, Created)
01-NOY-1998 (TremBLrel. 08, Last sequence update)
01-NOY-1999 (TremBLrel. 12, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LT 13
Q44769
SEQUENCE FROM N.A.

CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,
LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN I
DOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D.,
PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANSON M.
VAN-YUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J.,
UTTERBACK T., WATTHEY L., MCDONALD L., ARTIACH P., BOWMAN C.,
UTTERBACK T., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,
SMITH H.O., VENTER J.C.;
SUDMITTED (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                 FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,
LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN
DOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D.,
PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANSON M.
VAN-VUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J.,
UTTERBACK T., WATTHEY L., MCDONALD L., ARTIACH P., BOWMAN C.,
GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,
SMITH H.O., VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00046; homeobox; 1.
Homeobox; DNA-binding; Nuclear protein.
SEQUENCE 387 AA; 41738 MW; C862A1E0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: NUCLEAR EMBL; AF092538; AAC61772.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAKAHASHI M., TAMURA K., BUSCHER D., MASUYA H., YONE MATSUMOTO K., NAITOH-MATSUO M., TAKEUCHI J., OGURA R OGURA T., IZPISHUA BELMONTE J.C.;
"Strong's luxoid (lstD), a 16 base pair deletion in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Neognathae; Galliformes; Phasianidae; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
PAIRED TYPE HOMEODOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Development 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                      "Genomic sequence of a Lyme disease spirochaete, burgdorferi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi (Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          Nature 390:580-586(1997).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSFTMDLSELDIQEKFLKTTHSSHSGGLVSTMVKGTDNSNDAIKRALNKIFANI-MQEID 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPSGMDSSYLSVKEAGVKVPQDRASTDLPSPMDKADSESNKGKKRRNRTTFTSYQLEELE 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKLTQKNL-ESYQKDAKELK 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVFQKTHYPDVYAREQLAMR 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P06601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 6.6%;
Similarity 25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
98065943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00027; HOMEOBOX_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08, Created)
08, Last sequence update)
12, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease spirochete).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 105; DB 13;
Pred. No. 1.26e+00;
20; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H., YONEI-TAMURA OGURA K., SHIROJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                             Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      HANSON M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
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IRESULT
AC 077
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    SSEEPPP B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DUNN J.J., BUTLER-LOFFREDO L., K
Submitted (DEC-1995) to the EMBL
EMBL; AE001137; AAC66663.1; -.
EMBL; U43739; AAA85608.1; -.
HSSP; P13466; 1KSR.
TIGR; BB0285; -.
                                                             JLT 15
Q94895;
Q94895;
O1-FEB-1997 (
O1-FEB-1997 (
O1-NOV-1998 (
YOLK PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                077338;
077338;
01-NOV-1998
01-NOV-1998
01-NOV-1999
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DUNN J.J., BUTLER-LOFFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMLIN N., LAWSON D., BARRELL B.; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases EMBL; AL008970; CAA15593.1; -
  Eukaryota;
                    Drosophila mimica (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                        164
                                                                                                                                                                                                                                                                                                                                                                                                                                               106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFC0565W PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                           821
                                                                                                                                                                                                                                                                                                                                                                                                 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        703
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                                                                                                                                                                                                                                                                  223
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                                                                                                                                                                                                                                                                  ALNKIF
                                                                                                                                                                                                                                                                                                             SLINLF 826
                                                                                                                                                                                                                                                                                                                                                        - IKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGLVSTMVKGTDNSNDAIKR
                                                                                                                                                                                                                                                                                                                                                                                             DLILTNFEKKRNDFLQEFS-NLFN-DIPIIFLNTKNNTHINTLLNKIIHIHKMNNVIIST 820
                                                                                                                                                                                                                                                                                                                                                                                                                                          KDDFSFAQKKEGYLAVAMNGE-IVLRPDPKRTIQ-KKSEPGLLFSTGLDKMEGVLIPAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEDLLFDENNRYTNIRKSDICIYIKEIKNNNINLNKVDKKMIFYLLKEKKNIIFIVNKI 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPKRTIQKKSEPGLLFSTGLDKMEGVLIPAGFIKVTILEPMSGESLDSFTMDLSELDIQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EYENKFKNOTALKVEQILQNQGYKVISVDSSDKDDFSFAQK-KE-GYLAVAMNGEIVLRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 6.6%;
Similarity 19.8%;
25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l falciparum.
Alveolata; /
                                                                                 3 (TrEMBLrel.
3 (TrEMBLrel.
9 (TrEMBLrel.
Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394 AA;
                                                                                                                                                                                                                                                                  228
                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108563 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45073 MW;
  Arthropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apicomplexa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.A.
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12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 105; DB 5;
Pred. No. 1.26e+00;
43; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44;
                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 106; DB 2;
Pred. No. 9.65e-01
                                                                                      Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                    (Idiomyia mimica).
                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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arch completed: Tue Sep 26 16:20:56 2000
b time : 25 secs.
                                                                                                                                                                               Ouery Match 6.5%;
Best Local Similarity 29.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                         Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U51875; AAC47246.1; -.
FTYBASE; FB900016257; Dmic\Yp1.
FFAM; PF00151; lipase; 1.
NON_TER 1 1 1
NON_TER 272 272
SEQUENCE 272 AA; 30187 MW; DF3EFC7C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. HO K.F.;
                                                                              SEQUENCE FROM N.A.

MEDLINE; 96120851.

KAMBYSELLIS M.P., HO K.F., CRADDOCK E.M., PIANO F., PARISI M.,

COHEN J.;

"Pattern of ecological shifts in the diversification of Hawaiian

Drosophila inferred from a molecular phylogeny.";

Curr. Biol. 5:1129-1139(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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272 272
272 AA; 30187 MW; DF3EFC7C CRC32;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Tue Sep 26 16:16:34 2000; MasPar time 23.61 Seconds 684.174 Million cell updates/sec

Description: Perfect Score: Title:

Sequence: >US-09-308-435-2 (28-260) from US09308435.pep 1594 1 CSPHIIETNEVALKLNYHPA......CKNLESYQKDAKELKGKRNR 233

Scoring table: PAM 150 Gap 11

Post-processing: Minimum Match 0% Listing first 45 summaries Database:

Searched:

225878 seqs, 69334122 residues

sptremb112
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 46.291; Variance 102.838; scale 0.450

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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PECOSEM PROTEIN.  PECOSEM PROTEIN.  Y18D10A.11 PROTEIN.  FLAGELLAR PROTEIN (FLB SUGAR TRANSPORTER.  CEOB. CHROMOSOME X READING F FTSA.  SIMILAR TO CCAAT/ENHAN ENDO-1.4 -BETA GLUCANAS CELLOBIOSE DEHYDROGENA OUTER SURFACE PROTEIN INVASIN.	NEURAMINYLLACTOSE-BIND PUTATIVE PARALOG OF HP PUTATIVE NEURAMINYLLAC PUTATIVE PARALOG OF HP HYPOTHETICAL 31.9 KD P COMPLETE NUCLECTIDE SE PFC0895W PROTEIN.	Description
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## ALIGNMENTS

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Matches
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Best Local
TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G., PLEISCHAANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S., LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A., MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K., MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K., DERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., RELLEY J.: COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATTHEY L., WALLI CATTON M.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TIEMBLIEL. 05, Created)
01-JAN-1998 (TIEMBLIEL. 05, Last sequence update)
01-NOV-1998 (TIEMBLIEL. 08, Last annotation update)
PUTATIVE NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ HO
HP0410.
                                                                                                                                                                                                                      MEDLINE; 97394467.
                                                                                                                                                                                                                                                STRAIN-26695
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision;
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                                                                                                                                                                                                                                                                                                                       Helicobacter.
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Nature 397:176-180(1999).
EMBL; AE001526; AAD06549.1; -.
SEQUENCE 249 AA; 28513 MW; A3729951 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALM R.A., LING L.-S.L., MOIR D.T., KING B.L., BROWN E.D., DOIG P.C., SMITH D.R., NOONAN B., GUILD B.C., DEJONGE B.L., CARMEL G., TUDMINO P.J., CARUSO A., URIA-NICKELSEN M., MILLS D.M., IVES C., GIBSON R., MERBERG D., MILLS S.D., JIANG Q., TAYLOR D.E., YOVIS G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TEMBLIEL 10,
01-MAY-1999 (TIEMBLIEL 10,
01-MAY-1999 (TIEMBLIEL 10,
PUTATIVE PARALOG OF HPAA,
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VLIPAGFIKVTILEPMSGESLDSFTMDLSEL-DIQEKFLKTTHSSHSGGLVS-TMV-KGT 213
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Similarity 25.1%;
57; Conservative
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Pred. No. 1.92e-18;
74; Mismatches 74;
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Q9ZLY2;
01-MAY-1999
01-MAY-1999
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE001479; AAD06033.1; -. SEQUENCE 282 AA; 32075 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genomic-sequence comparison of two unrelated gastric pathogen Helicobacter pylori."; Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALM R.A., LING L.-S.L., MOIR D.T., KING B.L., BROWN E.D., DOI SMITH D.R., NOONAN B., GUILD B.C., DEJONGE B.L., CARMEL G., TUMMINO P.J., CARUSO A., URIA-NICKELSEN M., MILLS D.M., IVES GIBSON R., MERBERG D., MILLS S.D., JIANG Q., TAYLOR D.E., VOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRUST T
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01-MAY-1999 (TIEMBLIEL 10,
01-MAY-1999 (TIEMBLIEL 10,
PUTATIVE PARALOG OF HPAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALM R.A., LING L.-S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-J99
                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 99120557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   delicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori J99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JHP0444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein. SEQUENCE 249 AA; 28349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000557; AAD07478.1;
TIGR; HP0410; -.
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Nature 388:539-547(1997)
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                                                                                                                                                                                                              39
                                                                                                                                                                                                                              210 V-KGTDNSND-AIKSALNKIFANIMQEIDKKLTQKNLESYQKDAKELKGKRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 DKMEGVLIPAGFIKVTILEPMSGESLDSFTMDLSEL-DIQEKFLKTTHSSHSGGLVS-TM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94
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VLIPAGFIKVTILEPMSGESLDSFTMDLSELD-IQEKFLKTTHSSHSGGLVSTMVKGT-D
                                           VDQSSGSVWFNFYEPESNRVVHDFAVEVGTFQAITYTYTSTNNASGGFNSSKSVIHENLD
                                                                                               KVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEG
                                                                                                                                         QVLRFQD-EKA-LNVQDKKKIFSVLDLKGWVGILEDLKMNL--K-DPN---SPNLDTL--
                                                                                                                                                                                               ALKLNYHPASEKVQA-LDEKIL-LLRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKYID-M-SSGYLNLNFVEPKSEDIIHSFGIDVSKIKAVIER-VEL-RRTNSGGFVPKTF 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERKGYSV-S-QFKDASEIPQDIKEKALLVLRMDGNVAI-LE-D-IVEE-SDA--L-S-E- 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETNE-VALKLNYHPASEKVQALDEK-ILLLRPAFQYSDNIAKEYENKFKNQTALKVEQIL
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                                                                                                                                                                                                                                                                                                         h 10.7%;
Similarity 25.1%;
56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 13.9%;
Similarity 25.0%;
58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                 Score 171; DB 2; Le
Pred. No. 1.99e-09;
58; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation updat
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Pred. No. 3.51e-17;
74; Mismatches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                      E982253F CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       282
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                                                                                                                                                                                                                                                                                                    Indels 18;
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                                                                                                                                                                                                                                                                                                 Gaps
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Matches
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SEQUENCE FROM N.A.
ALONSO J.C., LUDER G., STII
Submitted (MAX-1996) to the
EMBL; X97918; CAA66554.1; .
SEQUENCE 179 AA; 20956 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pylor1.";
Nature 388:539-547(1997).
EMBL; AE000564; AAD07568.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE; 97394467.

TOMB J. *F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G., FLEISCHMANN R.D., KETCHUM K.A., KLENK H. *P., GILL S., DOUGHERTY B.A. FLEISCHMANN R.D., KETCHUM K.A., KLENK H. *P., GILL S., DOUGHERTY B.A. NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S., NELOTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A., MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K., MCKENNEY K., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M., COTTON M.D., WEIDMAN J.M., FUJII C., BOMMAN C., WAITHEY L., WALLIN E HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    025234
025234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. SEQUENCE 278 AA; 31947 MW;
                                                                                                    Bacteriophage SPP1
Viruses; dsDNA viruses,
                                                                                                                                    COMPLETE NUCLEOTIDE SEQUENCE.
                                                                                                                                                  01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-AUG-1998 (TrEMBLrel. 07,
                                                                                                                                                                                                                048453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR; HP0492; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hellcobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Hellcobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                               048453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'The complete genome sequence of the gastric pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter.
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                                                                                         ambda phage
                                                                                                                                                                                                                                                                     214 D-NSNDAIKSALNKIFANIMQEIDKKLTQKNLESYQKDAKELKG
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                                                                                                                                                                                                                                                                                                                                                  VDQSSGSVWFNFYEPESNRVVHDFAVEVGTFQAM-TY-TYKHN-NSGGLNSSNSIIHEYL
                                                                                                                                                                                                                                                                                                                                                                                            KVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEG
                                                                                                                                                                                                                                                                                                                                                                                                                       QVLRFQD-EKA-LNAQDKRKIFSVLDLKGWVGILEDLKMNL--K-DPN---NPNLDTL-- 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -NSNDAIKSALNKIFANIMQEIDKKLTQKNLESYQKDAKELKG
                                                                                                                                                                                                                                                                                                                                  VLIPAGFIKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGL-VS-TMVKG-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALKLNYHPASEKVQA-LDEKIL-LLRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
56; Conser
                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                        group
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                                            STIEGE A.C.,
                                the
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   WW;
                                                                                                       RNA
                                                                                                                                              Created)
Last sequence update)
Last annotation updat
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Last annotation updat
                              EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 161; DB 2;
Pred. No. 5.54e-08;
61; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                     stage;
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   85120A6C CRC32
                                                                                                                                                                                                             179
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                                                                                                    phages;
                                            WEISE
                                databases
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E
                                                                                                     Siphoviridae
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                                            TRAUTNER
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Query Match
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Matches 2
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Best Local
                                                                                     "Nucleotide sequence of the 3'-terminal two-thirds leafroll-associated virus-3 genome reveals a typica closterovirus.";
J. Gen. Virol. 79:1299-1307(1998).
EMBL; AF037268; AAC40708.1;
SEQUENCE 549 AA; 59013 MW; 2B128E62 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OLIVER K., BOWMAN S., HARRIS D., LAWSON D., QUAIL M., B SUBMITTED (FEB-1999) to the EMBL/GenBank/DDBJ databases EMBL; AL034559; CAB3907.1; -. SEQUENCE 578 AA; 68384 MW; 1AC1C75C CRC32;
                                                                                                                                                                                                                                    LING K.-S., ZHU H.-Y., DRONG R.F., SLIGHTOM GONSALVES D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                         STRAIN-NY
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          grapevine leafroll-associated virus 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998
01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-3D7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFC0895W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFC0895W PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 DKK-LTQKNLESYQKDAKELKGKRN 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 7.3%;
Local Similarity 24.7%;
hes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                               losterovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EYEKYKKKMKEKSMEMDMDNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKVQALDEKILLLRPAFQ-YSDNIAKEYENKFKNQTALKVEQILQNQGYKVISVDSSDKD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKTNSLEETLVQINNEYNKCIDMIEKEIHDNIDDKESLKVKNELEKL-C-VIKKEKDEKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEKELVLRGMEQY-KEIKKIREEMN 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLDSFTMDLSELDIQEKFLKTTHSSHSGGLVSTMVKGTDNSNDAIKSALNKIFANIMQEI 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLDDIGQALSDMDIDEAFNQAFQALDNSGFFKRAVRAYWKKNDSIIKALESQ-AKTIEDV 146
  Similarity
24; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 8.4%;
Similarity 28.2%;
24; Conservative
                                                                                                                                                                                                                                                                                  98264508.
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6.8%;
larity 24.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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12,
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08,
Score 109; DB 1
Pred. No. 4.25e-
30; Mismatches
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Last sequence update)
Last annotation updat
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22; 1
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Pred. No. 2.97e-04;
26; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 117; DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 4.54e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemosporida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       578
                          DB 14;
.25e-01;
                                                                                                                                                                                                                                                                                                                                                                                                  no DNA stage;
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                                                                                                                                                                                                                                                       J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                  typical
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                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium.
                                                                                                                                                                                                                                                          MCFERSON J.R.,
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  Closteroviridae;
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                                                  549;
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DPVETDVAQFNLSTDGTVSVIVNGEEV-KNEYLVPGTTNVLDSLVYKSGREDLEAKAIPE 502

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01-NOV-1999 (TrEMBLrel. 1
01-NOV-1999 (TREMBLREL. 1
01-NOV-1999 (TREMBLREL. 1
Y18D10A.11 PROTEIN.
Y18D10A.11
WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAYELLO A., FULTON L.,
GARDNER A., GREEN P., HAWRINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTLANGE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPA A., SAUUDERS D., SHOWNKEEN )
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (Trem
01-NOV-1998 (Trem
01-NOV-1999 (Trem
PFC0565W PROTEIN
                                                                                                                                                                                                                    MEDLINE; 94150718.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                  Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                               "2.2 Mb of contiguous nucleotide sequence
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhabditina; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9XW20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMLIN N., LAWSON D., BARRELL B.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AL008970; CAA15593.1; -.
SEQUENCE 911 AA; 108563 MW; 5043B736 CRC32;
                                                                                                                                                                                                                                                                                                                                                            HARRIS B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-3D7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFC0565W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 - IKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGLVSTMVKGTDNSNDAIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 KDDFSFAQKKEGYLAVAMNGE-IVLRPDPKRTIQ-KKSEPGLLFSTGLDKMEGVLIPAGF 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               703 NEDLLFDENNRYYTNIRKSDICIYIKEIKNNNINLNKYDKKMIFYLLKEKKNIIFIVNKI 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 6.8%;
Local Similarity 19.8%;
les 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLLNLF 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YLTTLNILHDKAFTRRNLGNKDKGFSDLRIEENFLKSA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLILTNFEKKRNDFLQEFS-NLFN-DIPIIFLNTKNNTHINTLLNKIIHIHKMNNVIIST 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALNKIF 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GFIKVTIL-E-PMSGESLDSFTMDLSELDIQEKFLKTT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 08, Created)
(TrEMBLrel. 08, Last sequence update)
(TremBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                  pda; Secernentea; Rhabditia; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 109; DB 5; Le
Pred. No. 4.25e-01;
44; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                    from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
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Best Local S
Matches 2
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01-NOV-1996;
01-NOV-1998;
01-NOV-1999
                                                DUNN J.J., BUTLER-LOFFREDO L., Submitted (DEC-1995) to the EMEMBL; AE0001137; AAAC66663.1; -- EMBL; U43739; AAA85608.1; -- HSSP; P13466; 1KSR.
                                                                                                                                                                                   FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,
LATHICEAR R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN M
DOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D.,
PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALIZBERG S., HANSON M.,
VAN-YUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J.,
UTIERBACK T., WAITHEY L., MCDONALD L., ARTIACH P., BOWMAN C.,
GARLAND S., FUJII C., COTTON M.D., HONST K., ROBERTS K., HATCH B.,
SMITH H.O., VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                ERASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,
LATHICRA R., WHITE O., KETCHUM K.A., DODSON R. HICKEY E.K., GWINN M
DOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D.,
PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALIBBERG S., HANSON M.,
VAN-YUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J.,
UTTERBACK T., WATTHEY L., MCDONALD L., ARTIACH P., BOMMAN C.,
GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,
GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,
"Genomic sequence of a Lyme disease spirochaete, Borrelia
"Genomic sequence of a Lyme disease spirochaete, Borrelia
   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 98065943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 11
Q44769
                                                                                                                                                                         Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                       Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLAGELLAR PROTEIN (FLBC) (ORF20).
                                                                                                                                              SEQUENCE OF 3-394 FROM N.A.
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 MSGE-SIDSFTMDLSELDIQEKFLKTTHSSHSGGLVSTMVKGTDN-SNDA-IKSALNKIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 ANIMQEI 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 QDAEVSMTTLKETVAKLEEENNVLQATWAEERSGLVNELIDTKEKLAKSAQAQTELDESH 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 QKK-EGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEGVLIPAGFIKVTILEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 RDIMTAV 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 QKRWEGELASSRAQNEQL-SEEKSQLQKENE-ELLLVL-L-RTEGIVDANKSLSEQLANA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity hes 28; Conser
                                  BB0285;
   394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P. contiguous nucleotide sequence from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrembLrel. 01, Created)
(TrembLrel. 08, Last sequence up
(TrembLrel. 12, Last annotation
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ilarity 22.0%;
Conservative
   AA;
 45073 MW;
                                                                                           i., KIELECZAWA J.,
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 105; DB 5; Lo
Pred. No. 1.26e+00;
40; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
5BF8FA60 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC3B5F9C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                             MEDALLE J., databases.
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Query Match Best Local :

Similarity

6.6%; 19.7%;

Score 106; DB 2; Pred. No. 9.60e-01

Length 394;

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Best Local (
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006471;
006471;
01-JUL-1997
01-JUL-1997
01-NOV-1999
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01-JUL-1997
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UT 12
005176
                  Sugar transport.
SEQUENCE 512 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             KEMNER J.M., LIANG X., NESTE:
J. Bacteriol. 179:0-0(0).
EMBL; U91632; AAB51510.1; -.
PFAM; PF00005; ABC_tran; 2.
                                                                                          Burkholderia cepacia (Pseudomonas cepacia). Bacteria; Proteobacteria; beta subdivision; Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agrobacterium tumefaciens. Bacteria; Proteobacteria;
                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobiaceae;
                                                                                                                                                                                                                                                                                      353
                                                                                                                                                                                                                                                                    156
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                                                                                                                                                                                                                            215
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                                                                                                                                                                                                                                                                                                                              295 IAGLMGAGRTEFAMSVFGKSY-GHRITGDVLIDGKPVDVSTVRKAIDAGLAYVTE-DRKH 352
                                                                                                                                                                                                                                                                                                            98
                                                                                                                                                                                                                                                                                                                                             6.6%;
Local Similarity 21.2%;
nes 29; Conservation
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                                                                                                                                                                                                                                      GGNQQ-KVVLSKWLFSN 426
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                                                                                                                                                                                                                                                                                                         VISVDSSDKDDFSFAQKKEGYLAVAMNGEIVL--RPDPKRTIQKKSEPGLLFSTGLDKME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPKRTIQKKSEPGLLFSTGLDKMEGVLIPAGFIKVTILEPMSGESLDSFTMDLSELDIQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EYENKFKNQTALKVEQILQNQGYKVISVDSSDKDDFSFAQK-KE-GYLAVAMNGEIVLRP
                                                                                                                                                                                                                                                                 -GVLIPAGFIKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGLVSTMVKGTD
 PR00702; AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193
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(TrEMBLrel. 04,
(TrEMBLrel. 12,
                                                                                                                                                                                    PRELIMINARY;
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ACRIFLAVINRP.
A; 110930 MW;
                                                                                                                                                                                                                                                                                                                                                                                            56512 MW;
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                                       BURNS J.L.;
ne EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha
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Last sequence
Last annotation
                                                                                                                                          Created)
Last sequence update)
Last annotation updat
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Pred. No. 9.60e-01;
45; Mismatches 54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            E.W.;
                                                                                                                                                                                                                                                                                                                                                                                            C6F6AEAC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subdivision; Rhizobiaceae
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 7C8108F2
                                                                                                                                                                                    1027
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                                                                                                  Burkholderia group;
                                                                                                                                           update)
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                                        databases
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Best Local Similarity 25.6%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.6%;
Best Local Similarity 14.5%;
Matches 21; Conservative
STRAIN=212;
MEDLINE; 97234641.
GE Y., OLD I.G., SAINT GIRONS I., CHARON N.
GE Y., OLD I.G., SAINT GIRONS I., CHARON N.
"Molecular characterization of a large Borr
operon which is initiated by a consensus si
J. Bacteriol. 179:2289-2299(1997).
EMBL; L76303, AABS1416.1; -.
HSSP; P13466; 1KSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7LT 15
Q44919
Q44919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CZIEPLUCH
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PR7192 PRELIMINARY; PRT; 1803 AA.

P87192; O1-JUL-1997 (TrEMBLrel. 04, Created)

O1-JUL-1997 (TrEMBLrel. 04, Last sequence update)

O1-JUL-1997 (TrEMBLrel. 04, Last annotation update)

CHROMOSOME X READING FRAME ORF YJL114W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases EMBL; Z49389; CAA89409.1; -.
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Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                          Borrelia burgdorferi (Lyme
Bacteria; Spirochaetales; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1231 DKNNSLTSYELERDKKRSKKNR 1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1171 NLKELKVTDKNVPTDNGTNVSPRLEQNIEASGSPVQTVNKSAFLNKEFSSLNMKRKRKRH 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLBC.
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                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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ZIEPLUCH C., KORDES
submitted (OCT-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 EIDKKLTQKNLESYQKDAKELKGKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TQKN-LESYQKDAKELKGKRNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.) (TrEMBLrel.)
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to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207693 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01,
12,
                                                                                                                                                                                                                                                                                                                                                                                              disease spirochete).
Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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Pred. No. 1.26e+00;
28; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 106; DB 2;
Pred. No. 9.60e-01
62; Mismatches 5
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                                                                                                                CHARON N.W.;
large Borrelia burgdorferi motility
nsensus sigma70 promoter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394
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databases.
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Run on: .Psrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Tue Sep 26 16:18:57 2000; MasPar time 8.99 Seconds 613.770 Million cell updates/sec

Title:
Description:
Perfect Score:
Sequence: >US-09-308-435-4 (28-260) from US09308435.pep 1599

1 CSPHIIETNEVALKLNYHPA.....QKNLESYQKDAKELKGKRNR 233

Searched: PAM 150 Gap 11

Scoring table:

188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq36 1:geneseqp

Statistics: Mean 32.470; Variance 175.985; scale 0.185

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

222118876554321 2221188765543221 2221188765543221	Result
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## ALIGNMENTS

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This polypeptide comprises a 29 kDa surface antigen which is campressed on the surface of both dividing (bacillary) and resting (colloid) forms of Helicobacter pylori. The antigen gives rise to both systemic and local (mucosal) production of antibodies. It is an adhesin that is conserved in all tested strains of H. pylori, and is also a putative virulence factor. The invention relates to negatively charged lipid or lipid mixture and at least one antigenic, native or recombinant antigen of H. pylori, preferably the surface-exposed 29 kDa antigen, or a nucleic acid (see vy4643) coding for such an antigen. The new formulations, which are useful as vaccine formulations, and are suitable for therapeutic and prophylactic use. An adequate response is produced even without adjuvant. A second, claimed 29 kDa antigen (see W60156) is provided that differs only at residue 222 (Ser for Arg).
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Matches 23
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Cell surface antigen; adhesin; infection; vaccine; drug delivery.
Helicobacter pylori.
W09822135-A1.
28-MAY-1998.
18-NOV-1997; SE1927.
22-NOV-1996; SE-004000
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TMVKGTDNSNDAIKRALNKIFANIMQEIDKKLTQKNLESYQKDAKELKGKRNR
                                                       CSPHIIETNEVALKLNYHPASEKVQALDEKILLLRPAFQYSDNIAKEYENKFKNQTALKV
               TMVKGTDNSNDAIKRALNKIFANIMQEIDKKLTQKNLESYQKDAKELKGKRNR 260
                                                                                                                      POILQNQGYKVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLF
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98-312174/27.
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Pred. No. 2.57e-113;
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Helicobacter Antigen; adhesin; therapy; diagnosis

diagnosis.
cter pylori strain CCUG 178.
Location/Qualifiers

17874

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immunogen;

vaccine;

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immunisation; kDa

ulcer;

/label- Sig\_peptide 25. .28

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Cell surface antigen; adhesin; infection; vaccine; drug delivery.
Helicobacter pylori.
W09822135-A1.
28-MAY-1998.
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04-MAR-1997 (first
Helicobacter pylori
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Berglindh T, L,
WPI; 98-312174,
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Pred. No. 1.58e-112;
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CR A 29 kDa antigen (W07449) of Helicobacter pylori is an adhesin expressed on the surface of resting and dividing forms of the bacterium. It is conserved in all tested strains of H. pylori, and gives rise to both systemic and local (mucosal) prodn. of antibodies. Its amino acid sequence was deduced from a cDNA clone (T43834); a sequence (W07550) deduced from a second cDNA clone (T43835) differs only at position 222 (Arg for Ser). Recombinant antigen can be produced in transformed host cells. It is useful for the diagnosis and treatment of H. pylori infections and for series as a vaccine.
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  useful in
Claim 2; P
                                                                                                                                                                   duodenal ulcer.
Chimeric - Helicobacter pylori.
Chimeric - Vibrio cholerae.
Fusion gene consisting of the Helicobacter pylori adhesin ligated to the A2 and B subunit gene of Vibrio cholerae to useful in the diagnosis and treatment of H. pylori Claim 2; Page 20-21; 32pp; English.
                                                                         WPI; 98-434925/37.
                                                            N-PSDB; X21955
                                                                                     21-MAY-1997; 000091.
21-MAY-1997; WO-KR0091.
(DAEW-) DAEWOONG PHARM CO
Kim BO, Lee BK, Park SK, Y
                                                                                                                                                                                                                               Fusion gene, H.
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Adhesin/V.cholerae toxin A2 and B
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18-MAY-1999
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W74466 standard;
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Bolin I, Svennerholm A;
WPI: 97-034307/03.
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01-JUN-1995; SE-002007.
21-MAR-1996; SE-001085.
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larity 99.6%;
Conservative
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peptidase
28. .260
                                                                                                                                                                                                                                                                                       Protein;
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/note= "either the uncleaved or mature protein
be used in applns of the immontion
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                                                                                                                                                                                                                 infection;
diagnosis;
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                                                                                   Yoon
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Pred. No. 1.
0; Mismatc
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adhesin gene; V. cholerae toxin;
vaccine; gastritis; gastric ulcer;
                                                                                      Ϋ́u
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..58e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 260;
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RESULT ACC YILL YILL ACC YILL 
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Best Local S
Matches 23
     infections (laims 27, 31; Page 207-208; 279pp; English. Claims 27, 31; Page 207-208; 279pp; English. Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 73 ORFs are shown. The proteins are variously cell envelope proteins, secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life
                                                                                                                                                                                                                                                                                                                                                                                                                  wPI; 98-271811/24.
N-PSDB; X30467.
Helicobact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H. pylori ORF 11ap20714 4797137 f3_45
Vaccine; probe; diagnostic; ORF; cell
secreted protein; cellular protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and its ablility to stimulate sigA production. stimulate sigA production. Note: This sequence was indexed from WO' Note: This sequence was indexed from WO'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the fusion protein of the invention, between the H. pylori adhesin gene, and the V. cholerae toxin A2 and B subunit genes This protein is used in the diagnosis of and as a vaccine against H. pylori, which is the main cause of gastritis and gastric/duodenal ulcers. It may also be used in the production of an anti-H. pylori antibody. Vectors containing the DNA sequence and E. coli strains containing it form the basis of a process to produce the protein, which consists of culturing the microorganism and obtaining the protein. The protein is an effective vaccine against H. pylori due to its excellent immunogenicity for H. pylori, stability within the stomach environment, and its ability to penetrate through the stomach mucous membrane to
                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori nucleic acids and proteins -
products for the detection, prevention and treatm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori.
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14-JUL-1997; US-891928.
28-OCT-1996; US-739150.
06-DEC-1996; US-759739.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ASTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Pred. No. 1.58e-112;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                and treatment
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                                                                                                                                                                                                                            Helicobacter pylori nucleic acid sequences and related PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori PT infection, and to detect Helicobacter

PT infection, and to detect Helicobacter

BS Disclosure; Page 1363-64; 1481pp; English.

CC This sequence represents a H. pylori protein.

CC This sequence represents a H. pylori protein.

CC Infection or to identify H. pylori polypeptide binding compounds,

CC useful as potential H. pylori life cycle activators or inhibitors.

CC The genomic sequence of H. pylori (ATCC 55679) was determined from

CC overlapping contigs generated by mechanically shearing the bacterial

CC DNA. The sequences were analysed for ORF of at least 180 nucleotides,

and the predicted coding regions defined by computer evaluation. To

identify likely H. pylori antigens for vaccine development, the amino

acid sequences predicted from various ORF were analysed for significant

homology to other known or exported membrane proteins. Having identified

CC isolated from H. pylori by PCR amplification for recombinant polypeptide

CC production, e.g. in E. coli hosts.
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06-JUN-1996; U09122.
07-JUN-1995; US-487032.
01-APR-1996; US-630405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic; vaccine; prevention; treatment; identification; binding compound; bacterium; bacteria; inhibitor; duodenal ulcer disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; T68226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ASTR ) ASTRA AB.
Berglindh OT, Sm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis.
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                                                                                                                                                                                     96.3%;
95.3%;
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                                                                                                                                                                     Score 1540; DB 1;
Pred. No. 1.14e-108;
7; Mismatches 4;
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life cycle; activator;
chronic gastritis;
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                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents an H. pylori derived protein, no further details are given in the specification.

C details are given in the specification.

C Helicobacter pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleic acid sequences of the invention are used to evaluate compounds, especially activators or inhibitors of bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequences. The nucleic acid sequences, and corresponding proteins, are also useful for generating vaccines for immunising subjects against H. pylori or in the indetecting the presence of Helicobacter species in a sample. Antisense nucleic acid sequences of these sequences are used to inhibit expression of a gene from Helicobacter species. H. pylori whole genomic DNA was isolated and nebulised to a median size of pylori whole genomic DNA was isolated and nebulised to a median size of pylori-linker adapters in 100-1000 fold molar excess. These linkers are complementary to the BstXI-cut pMPX vectors, while the overhang is not self-complementary. Then excepts in the content of the 20 pMPX vectors to construct a series of shotgun subclone libraries. The purified DNA samples were then
                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 4
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W24663;
W24663;
12-AUG-1997
        H. pylori derived protein.

Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
                                                                                29-JUL-1997
                                                                                                    W20454 standard; protein; W20454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori nucleic acid sequences and related proteins used for diagnostics and therapeutics Claim 18; Page 178; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; cytoplasmic; cell envelope; flagella; tran secreted; periplasmic; chronic gastritis; duodenal ulcer activator; inhibitor; bacterial life cycle; vaccine; immu detection; antisense; inhibition.
                                                                                                                                                                                                                                                                                                                            Note: The ORF/protein reference number for this sequence was obtained from the related specification, W09640893.
Sequence 97 AA;
   Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-NOV-1996; U18542.
17-NOV-1995; US-561469.
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                                                                                                                                                                                 TMVKGTDNSNDAIKSALNKIFASIMQEMDKKLTQRNLESYQKDAKELKNKRNR
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43; Conser
                                                                                                                                                                                                                                                        18.9%;
larity 97.7%;
Conservative
                                                                                  (first entry)
   pylori
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Pred. No. 5.
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5.74e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pf Helicobacter pylori nucleic acid sequences and related problypeptide(s) - useful for vaccines to treat or prevent H. pylori finfection, and to detect Helicobacter

pisclosure; Page 655; 1481pp; English.

The present sequence is a H. pylori derived protein, no further details are given in the specification.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, the protein may be used in a vaccine to prevent or inhibitors.

The protein may be used in a vaccine to prevent or inhibitors.

The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
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Best Local :
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09-OCT-1997; U05223;
27-MAR-1996; US-761318.
29-MAR-1996; US-625811.
02-APR-1996; US-738731.
25-OCT-1996; US-738959.
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06-JUN-1995; US-487032.
07-JUN-1995; US-487032.
01-APR-1996; US-630405.
        Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection Claims 14,80; Page 653; 1145pp; English.

This sequence is a H. pylori cell envelope outer membrane protein The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors.

DNA and probes derived from it may be used for the identification (
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W55445;
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                                                                                                                                                                                                                                                                       N-PSDB; V24854.
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m RA, Smith D;
'I; 97-503122/46.
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larity 97.7%;
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.74e-13;
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g compounds,
inhibitors. The
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PI Alm RA, Smith D;

DR WPI; 97-503122/46.

DR WPI; 97-503122/46.

DR WPI; 97-503122/46.

DR WPI; 97-503122/46.

PT polypeptide(s) - useful in vaccines to treat or prevent H. pylori polypeptide(s) - useful in vaccines to treat or prevent T. pylori infection

PT infection and for diagnosis of H. pylori infection

Claim 14; Pages 558-559; 1145pp; English.

CC This sequence is a H. pylori protein of unspecified function.

CC The protein may be used in a vaccine to prevent or treat H. pylori CC infection or to identify H. pylori polypeptide binding compounds, cuseful as potential H. pylori life cycle activators or inhibitors. The CC Useful as potential H. pylori life cycle activators or inhibitors. The CC Useful and probes derived from it may be used for the identification of CC H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic
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09-CT-1997; U05223;
27-MAR-1996; US-761318.
29-MAR-1996; US-625811.
02-APR-1996; US-758731.
25-CCT-1996; US-736905.
28-CCT-1996; US-738859.
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H. pylori ORF hp3el1075orf3 protein.
Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
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Misc_difference
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15-JUN-1998
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llarity 25.1%;
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are not given in the specification"
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Pred. No. 3.94e-08;
75; Mismatches 73;
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01-APR-1998; U06371.

29-JUL-1997; US-902615.

01-APR-1997; US-833457.

24-JUN-1997; US-881227.
                                                                         New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases Claim 8; Page 455-456; 2054pp; English.

This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating the inventions, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for the production of antibodies. The products can also be used for the production of antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and distribution of H. pylori-specific antigens. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR ammificant homology can be isolated from H. pylori by PCR ammificant homology to other known or exported membrane proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptic ulcer disease
Helicobacter pylori.
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                                                                                                                                                                                                                                                                                                                        N-PSDB; X14051
                                                                                                                                                                                                                                                                                                                                        Al-Garawi A, Kleanthous WPI; 98-542293/46.
                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
(INNR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
Al-Garawi A, Kleanthous H, Miller C, Oomen RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9843478-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W98332 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 SV-S-QFKDVSEIPQDIKEKALLVLRMDGNVAI-LE-D-IVEE-SDA--L-S-E-EKVID 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 VELHFHY-PIKGKQEPKNNHLVVLIDPKIEANKVIPENYQKEFEKSLFLQLSNFLERKGY 110
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les 57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ylori GHPO 1615 protein.
protein; Helicobacter infection;
ic_ulcer disease.
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      Similarity
58; Conse
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larity 25.0%;
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larity 25.1%;
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PO 1615 protei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
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Score 227; |
Pred. No. 1.,
75; Mismatcl
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Pred. No. 3.94e-08;
75; Mismatches 73
e 227; DB 1; L4
. No. 1.46e-07;
Mismatches 76;
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                                    Length 249;
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06-DEC-1996; US-759;
(ASTR) ASTRA AB.
Alm RA, Smith D;
WPI; 98-271811/24.
N-PSDB; X30418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 73 ORFs are shown. The proteins are variously cell envelope proteins, secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori nucleic acids and proteins - products for the detection, prevention and treatm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JUN-1999 (titel envel)
H. pylori ORF 04ee11108 3906963_fl_7 cell envelope protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claims 27, 31; Page 151; 279pp; English
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07-MAY-1998.
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                                                                                                                                                                                                                                                                    QVLRFQD-EKA-LNVQDKKKIFSVLDLKGWVGILEDLKMNL--K-DDN---SPNLDTL-- 170
                                                                                                                                                                                                                         KVISYDSSDKDDFSFAQKKEGYLAVAMNGEIYLRPDPKRTIQKKSEPGLLFSTGLDKMEG 156
                                                                                                                                                                                                                                                                                                                                            ALKLNYHPASEKVQA-LDEKIL-LLRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY 96
-NSNDAIKRALNKIFANIMQEIDKKLTQKNLESYQKDAKELKG
                                                   KNREDAIHKILNRMYAVVMKKAVTELTKENIAKYRDAIDRMKG
                                                                                                                                                                VDQSSGSVWFNFYEPESNRVVHDFAVEVGTFQAITYTYTSTNNASGGFNSSKSVIHENLD 230
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Similarity 25:1%;
56; Conservation
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US-891928.
US-739150.
US-759739.
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cellular protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 176; DB 1; Le
Pred. No. 5.19e-04;
59; Mismatches 90;
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The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
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Best Local S
Matches 5
                                                                                                                                                               diagnosis.
Helicobacter p
W09640893-A1.
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07-JUN-1995;
01-APR-1996;
19-DEC-1996;
06-JUN-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                    H. pylori secreted or peripplsmic protein, 3906963.aa. Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter Claim 72; Page 1333-1334; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berglindh OT, Smi
WPI; 97-052306/05.
N-PSDB; T68191.
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Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; binding cycle; activator; bacteria; life cycle; activator; binding cycle; life cycle; activator; binding cycle; life cycle; life
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Similarity 25.1%;
56; Conservative
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This sequence represents a H. Pylori secreted or periplasmic protein. CC The protein may be used in a vaccine to prevent or treat H. Pylori infection or to identify H. Pylori polypeptide binding compounds, cc useful as potential H. Pylori life cycle activators or inhibitors. CC The genomic sequence of H. Pylori (ATCC 55679) was determined from coverlapping contigs generated by mechanically shearing the bacterial CC DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To cleantify likely H. Pylori antigens for vaccine development, the amino CC identify likely H. Pylori antigens for vaccine development, the amino CC acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be considered from H. Pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                             Query Match
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Berglindh OT, Sm
WPI; 97-052306/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; T67633.
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7.4%;
Local Similarity 28.1%;
hes 25; Conservative
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Score 118; DB 1;
Pred. No. 3.41e+00;
26; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences and cines to treat
                                      Length 147;
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